New capabilities in nirsLAB (v2014.05):

1. Revision v2014.05 of nirsLAB is a standalone package. It is no longer necessary for you to include NAVI and SPM8 in your MATLAB search path. It is not even necessary for you to have them on your computer at all.
2. The **Utilities** portal now includes a 'Raw data editor': This new tool allows users to down-sample their raw data files, or to remove time segments that they are not interested in processing. Both capabilities reduce the size of the data files, and down-sampling also has the effect of improving the signal-to-noise ratio.
3. The **Utilities** portal now includes a 'Batch process' tool: This new tool allows users to calculate the hemodynamic states for multiple subjects or recording sessions, in a batch processing way.
4. The **Data Preprocessing** portal now includes a *Check raw data* function: This new tool allows users to manually or automatically designate each data channel as either 'good' or 'bad', on the basis of the experimental gain setting or of the raw data's coefficient of variation.

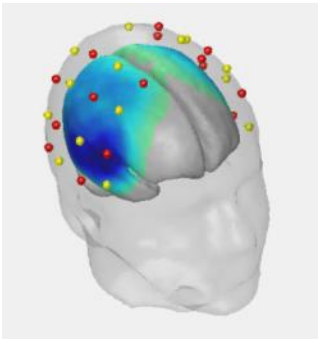
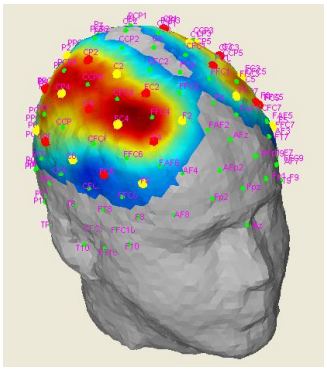
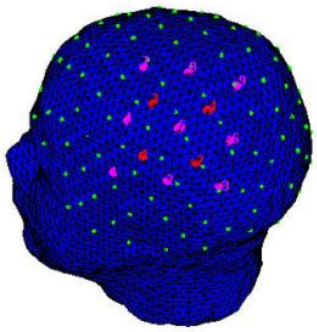
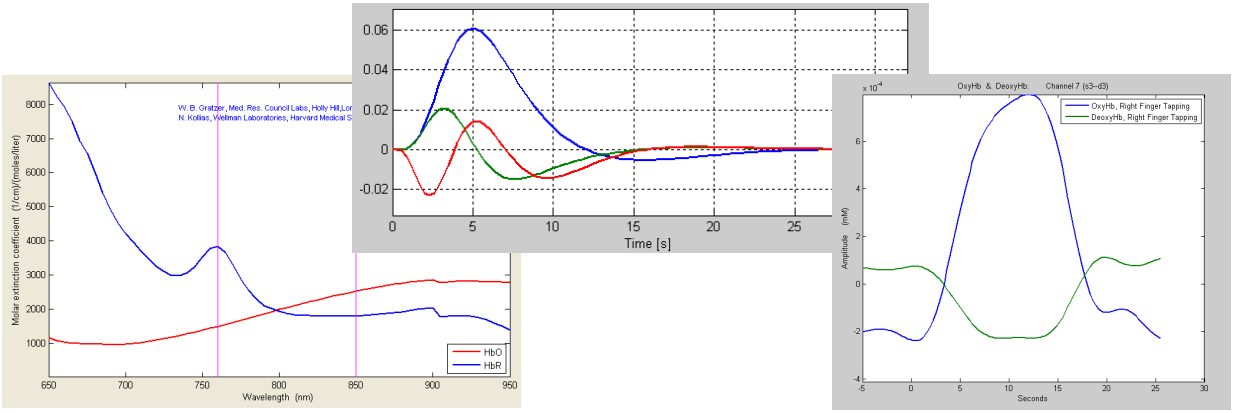
Modifications to algorithms and/or data structures:

1. When a user specifies one or more interior time segments for truncation (*Truncate Time series* functionality in the **Data Preprocessing** portal), nirsLAB now merges the data on the two sides of the deleted segments in a manner that avoids the introduction of jump discontinuities.
2. When data are frequency filtered (*Apply Frequency filter* functionality in the **Data Preprocessing** portal), nirsLAB now automatically saves a file containing the filtered data, in the *Detectors* sub-folder. This reduces the time delay that the user will experience while displaying the filtered time series data in the **Data Viewer** portal.
3. If the user loads a _config.txt file from a folder than already contains a _nirsInfo.mat file, nirsLAB now asks if the user really intends to overwrite the existing nirsInfo file. This is a protection against inadvertent loss of data-processing information that has already been generated.

Bug fixes:

Several user-reported bugs have been fixed in this release. The most serious one was that when users tried to sequentially process multiple data sets during a single nirsLAB session, the event-timing information did not always update correctly. Revision v2014.05 of nirsLAB correctly reads timing information, and users will no longer find it necessary to restart the application between successive data sets. (The other reported bugs were more minor, and included such things as misspelled words.)

nirsLAB

Chapter 1: Getting Started

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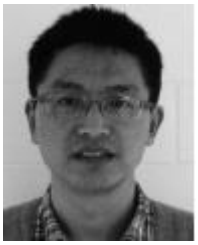
About the authors:



Dr. Yong Xu is the principal architect and programmer of nirsLAB. Dr. Xu received his Ph.D. degree in physics from the Southwest Jiaotong University, China in 1996. Following post-doctoral fellowships at the Institute of Applied Physics and Computational Mathematics in Beijing, China and subsequently Clemson University he joined the faculty at SUNY Downstate Medical Center in 2003 as Research Assistant Professor. Dr. Xu has more than 60 peer review and conference reports covering computational topics in image formation and algorithm development. Dr. Xu is also the Director of Software Development at NIRx Medical Technologies, Glen Head, NY. His research interest cover algorithms for diffuse optical imaging, optical signal processing, and application of optical methods applied to neuroimaging and breast cancer studies.

Dr. Harry Graber is responsible for code testing and algorithm validation and is principal author of the nirsLAB user manual. Dr. Graber received his Ph.D. degree in Physiology and Biophysics from SUNY Downstate Medical Center in 1998. Dr. Graber has published more than 100 peer review and conference papers describing systems level technology, algorithm and application development for methods used in 3D imaging of tissues using NIR optical sources. Dr. Graber is also Senior Applications Specialist for NIRx Medical Technologies.

Dr. Randall Barbour is Professor of Pathology and Bioengineering at the SUNY Downstate Medical Center and is Director of the Optical Tomography Group. He is an originator of the field of diffuse optical tomography and is co-founder of NIRx Medical Technologies, LLC. Dr. Barbour earned his Ph.D. degree in Biochemistry from Syracuse University and holds a professional license in Laboratory Medicine from the NYS Department of Health. Dr. Barbour has an extensive background in a broad range of medical, scientific and technical fields, has published more than 200 peer review and conference reports, has been awarded more than 20 patents and has been continuously funded by various federal agencies since 1993. Dr. Barbour is responsible for coordinating development of the nirsLAB software project.

1 Introduction

The nirsLAB package is a MATLAB-based versatile software analysis environment developed to support the study of time-varying near infrared measurements of tissue using the NIRScout, NIRSport, and DYNOT imaging systems. It is composed of modules for:

- Importing NIRS measurement data, along with relevant information regarding the measurement that was performed (*e.g.*, locations of optical probes [optodes] on the scalp, timing of applied stimuli or experimental tasks).
- Creating files that contain the optode-position and measurement-timing information together with toolboxes for editing this information.
- Preprocessing of measurement data using toolboxes that exclude data channels having excessive noise, deleting experimentally irrelevant time intervals, removing artifacts from data and filtering to exclude experimentally irrelevant frequency bands.
- Computing hemodynamic states using wavelength and path length dependent parameter settings.
- Visualizing the time series response of measurement data and computed hemodynamic states within a viewing formats (e.g., stacked, 2D, scalp and cortical).
- Extracting dynamic features from hemodynamic states by use of statistical parametric mapping methods (SPM) and mapping this information to head-space models.

These modules are linked to an automated file manager and a project-specific metadata ledger and provide you with abilities that are both convenient and powerful.

This chapter provides information about installing nirsLAB, its main components, preparing data and initializing projects.

1.1 Intended Readership

Familiarity with this document is strongly recommended for all users of NIRx imaging systems who intend to process data with nirsLAB. Permission to use content of this manual for educational purposes is available pending written approval from the SUNY Downstate Optical Tomography Group.

1.2 Related Documents

The following user manuals and documents may contain additional information pertinent to the subject matter of this manual:

- NIRStar 13.0 User Manual.
- User Manual for nilab2 Topographic NIRS Analysis Software

- NAVI (Near-infrared Analysis, Visualization, and Imaging) User Guide

1.3 Problem Reporting Instructions

You can contact NIRx for additional support and bug reports in either of the following ways:

E-mail: support@nirx.net

Web: www.nirx.net/contact-us

1.4 Public Access

nirsLAB, NAVI and Brain Model Generator are software products developed by the SUNY Downstate Optical Tomography Group. These can be accessed through:

http://www.nitrc.org/projects/fnirs_downstate

2 Installation

2.1 Contents in the nirsLAB Package

The nirsLAB package, which is freely available from the www.nitrc.org website (in fNIRS_Downstate), comprises three folders:

- nirsLAB_v01_p: a p-file version of nirsLAB v1.0;
- nirsLAb_demodata: contains NIRScout data sets for demonstration purposes;
- nirsLAB_manual: explains how to install and use nirsLAB.

2.2 System Requirements

- Intel I5 processor (or equivalent), or faster;
- Windows XP, 7 or later;
- At least 2 Gbyte RAM;
- 800 x 600, or higher , 16-bit display (32-bit recommended);
- This code has been developed under MatLab R2012a. Later versions are compatiable. MATLAB versions 2009-2012 may also be compatiable.
- At least 200 Gbyte available disk space.

2.3 Installation

To run the current release of nirsLAB, v1.0, it is necessary that you have the MATLAB application (R2012A is currently preferred), with the Image Processing, Signal Processing and Statistics toolboxes.

To install the p-file version of nirsLAB on your computer, please take the following steps:

1. Download nirsLAB, v1.0 from www.nitrc.org website (in fNIRS_Downstate).
2. Create a workspace for nirsLAB on one of your computer's hard drives (for example, C:\NIRXpackage\nirsLab\), and copy the entire nirsLAB package folder to that location.
3. Add the newly created folder to the MATLAB Search Path, as follows:
   a. Launch MATLAB.
   b. Select and click on *Set Path...* in the MATLAB *File* menu, or enter 'pathtool' at the MATLAB command prompt. This will open the *Set Path* GUI.
   c. Click on the *Add with Subfolders* button in the *Set Path* window. This will launch the *Browse For Folder* window. Navigate to the nirsLab_v01_p directory on your computer's hard drive. Select/highlight the nirsLab_v01_p folder and click on the *OK* button.
   d. Click on the *Save* button in the *Set Path* window, then on the *Close* button, and then exit from MATLAB.

3 Launching nirsLAB

Once nirsLAB is installed, simply enter 'nirslab' at the MATLAB command prompt to launch the nirsLAB home screen shown in Figure 1-1.

4 Main Components

4.1 File Manager and Electronic Ledger

When experimental data is processed, the nirsLAB computing environment automatically generates a hierarchical file structure for each project, and it simultaneously records all processing steps in an electronic ledger.

nirsLAB treats each NIRScout-, NIRSport-, or DYNOT-generated experimental data set as a distinct project. Loading raw data into nirsLAB immediately initializes the electronic ledger (saved in a special file having a name that ends with '_nirsInfo.mat'), which records information regarding the details of data collection, optode setup, and NIRS channel selection. Once initialized, the nirsInfo file keeps track of all facets of nirsLAB-based data processing. Meanwhile, the automated file manager creates a hierarchical tree structure for the project, and it subsequently uses information extracted from the nirsInfo file to

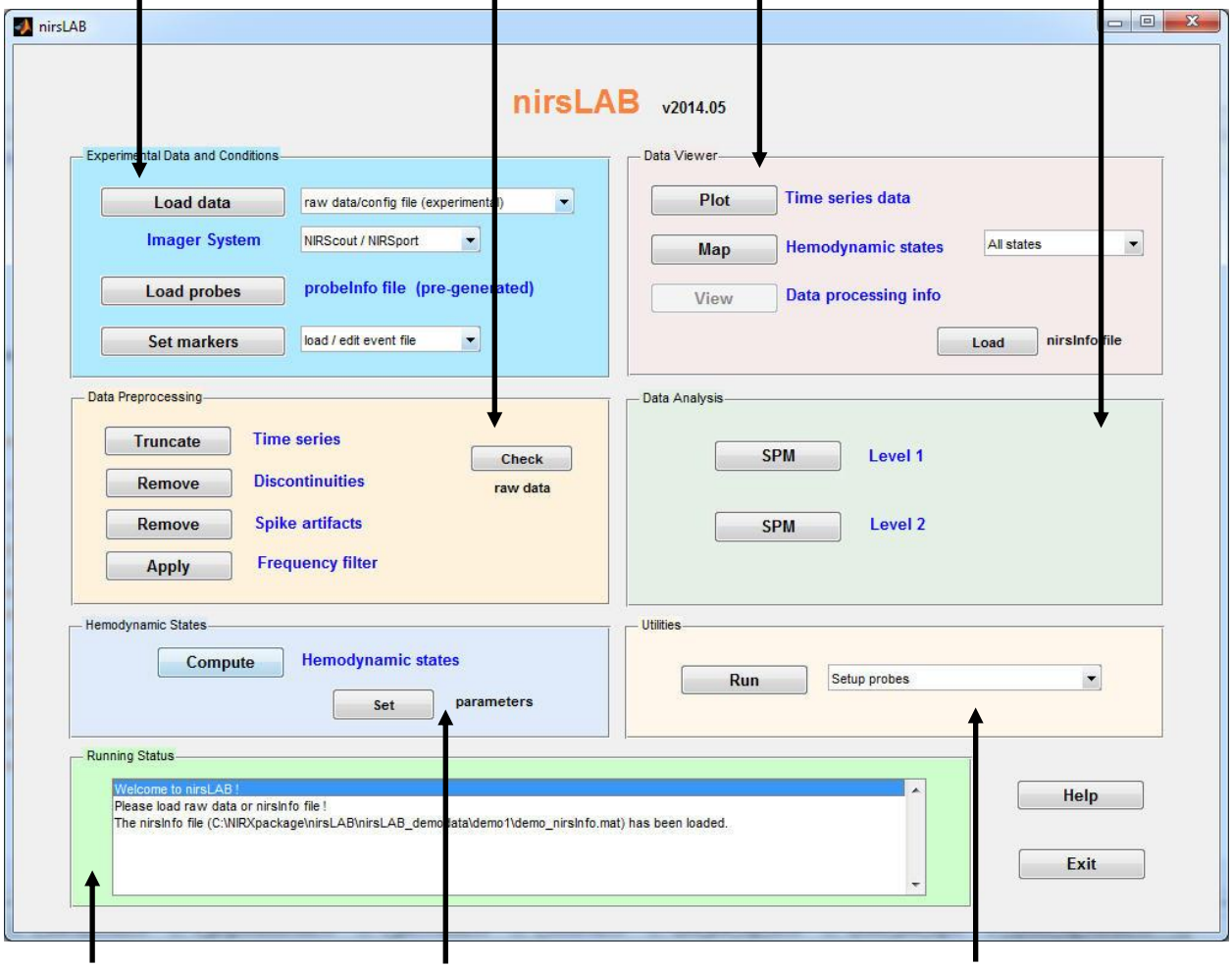
control file input and output. In combination, these abilities provide a single, easy-to-use mechanism for accessing all files associated with a project.

The *Experimental Data and Conditions* portal is used for loading data files, and the files that contain probe locations and experiment timings (Chap. 2).

Use the *Data Viewer* portal to plot data time series, map hemodynamic states onto a model brain surface, or review data-processing information (Chap. 5).

Use the *Data Preprocessing* portal to eliminate unwanted channels or time intervals, remove artifacts, and apply frequency filters (Chap. 3).

Use the *Data Analyzer* portal to perform Level-1 and Level-2 statistical analyses on hemodynamic states (Chap. 6).



The *Running Status* window displays the status of the operations that are being performed, in all data processing stages.

Use the *Hemodynamic States* portal to specify parameters for, and then to perform, hemodynamic-states computations (Chap. 4).

Use the *Utilities* portal tools to generate files that contain information on optical probe locations (Chap. 7), export nirsLAB-generated data to other file formats (Chap. 8), reduce the size of large data files (Chap. 9), or perform batch processing (Chap. 10).

Figure 1-1. Overview of nirsLAB main GUI.

4.2 nirsLAB Data-Processing Portals

Each of the data-processing tasks and functions mentioned in the Introduction is implemented in one or another of the nirsLAB portals, as indicated in Figure 1-1. Here we briefly describe the operations that may be performed in each portal, and indicate which chapter of this user's manual to see for more detailed information and instructions. Users may consult the other chapters in any order. We expect that you will find that for any particular data set you will choose to apply only a subset the capabilities provided by nirsLAB. Which ones will be appropriate in a given case will depend on your assessment of data quality, and on details of the experimental protocol.

4.2.1 Experimental Data and Conditions

The components of **Experimental Data and Conditions** (Chap. 2) allow you to: load experimental data files produced by a NIRx imager system (NIRScout, NIRSport or DYNOT) and then initialize a new nirsLAB project; load the nirsInfo file for an already-existing project, in order to review previously generated results or to perform additional data processing; import a previously generated file that contains optode-location information (see Chap. 7 for instructions on how to generate such a file in cases where it does not already exist); and import a previously generated file that contains information related to the timing of an experiment (*e.g.*, a listing of the experimental time intervals during which stimuli were presented), edit the timing information if necessary, or generate a timing-information file if one does not already exist.

4.2.2 Data Preprocessing

The components of **Data Preprocessing** (Chap. 3) allow you to: delete experimentally irrelevant time intervals from data; remove artifacts ("steps" and "spikes") from data; and apply band-, low- or high-pass frequency filters to exclude experimentally irrelevant frequency bands.

4.2.3 Hemodynamic States

The components of **Hemodynamic States** (Chap. 4) allow you to set parameters for Hb-concentration calculations, and then to compute the hemodynamic states (*e.g.*, concentrations of oxygenated, deoxygenated or total Hb; Hb oxygen saturation) by use of the Beer-Lambert Law.

4.2.4 Data Viewer

The components of **Data Viewer** (Chap. 5) allow you to: view time series for individual data channels (*i.e.*, source-detector pairs); generate block-averaged time-series data; topographically project the data onto models of head and brain surfaces; and examine the information included in the project-specific nirsInfo file (*under development*). In addition, if your inspection of data reveals that there are channels you want to exclude from further consideration (*e.g.*, because the data in them are excessively noisy), the **Data Viewer** provides a mechanism for excluding them.

4.2.5 Data Analysis

The components of **Data Analysis** (Chap. 6) allow you to extract event-related features from the hemodynamic-states time series, by use of Level-1 (typically, comparisons among different data channels within a single data set) and Level-2 (typically, comparisons across multiple subjects , where the same experimental protocol was applied to all) general linear model analyses.

4.2.6 Utilities

The **Utilities** portal contains two useful tools: *Setup probes* and *Data export*.

- The **Probe Setup** tool (Chap. 7) allows you to indicate where on the scalp the source and detector optodes were located during a particular measurement, and then to select which pairings of source and detector optodes constitute experimentally relevant channels during subsequent processing and display operations. The tool will generate a special file, having a name that ends with '_probeInfo.mat', that contains all information you specify. You can simply load the probeInfo file during subsequent nirsLAB sessions, and consequently you will not need to repeat the *Setup probes* operation.
- The **Data Export** tool (Chap. 8) allows you to export nirsLAB-generated information in other file formats, so it can be imported into other software applications.

5 Data Preparation

Some simple preliminary steps should be taken prior to using nirsLAB to initialize a new project. This section guides you through a checklist of steps that we recommend you take before attempting to load NIRScout-, NIRSport- or DYNOT-generated experimental data files with nirsLAB.

5.1 Experimental Data Files

In any measurement performed with a NIRx imager system (NIRScout, NIRSport, or DYNOT), the following files are produced:

- *filename*.wl1 [detector readings for wavelength 1 (760 nm)]
- *filename*.wl2 [detector reading for wavelength 2 (830nm, or 850 nm)]
- *filename*.set [gain-settings table]
- *filename*.evt [event records]
- *filename*_config.txt [information regarding experimental configuration]

Usually, *filename* is defined by the imaging system before the measurement starts, and it employs a syntax that uniquely identifies the experiment and the date on which the data were collected. However, as explained in the NIRStar 13.0 User Manual, the user is permitted to modify the imager-default

filename value. If you are attempting to process data that have a customized *filename*, note that the *filename* may not contain any blank spaces, or any other special character other than one or more underscores. If it does, it will not be accepted by nirsLAB.

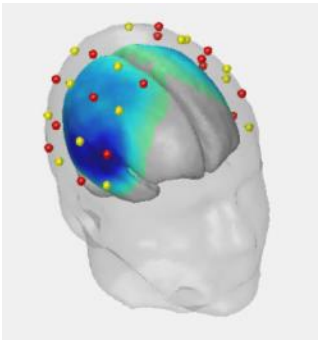
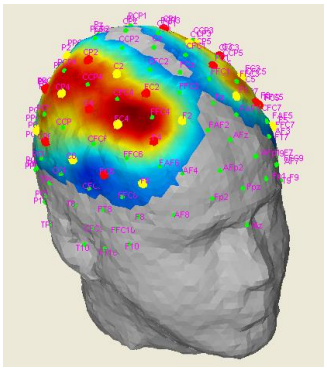
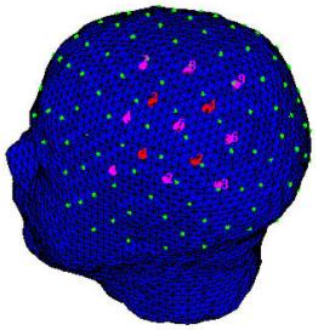
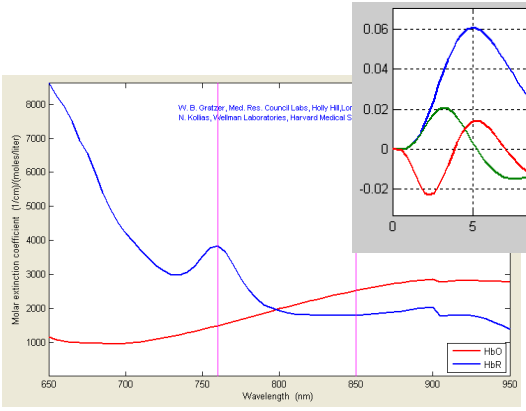
Note also that the special-characters caveat described in the preceding paragraph applies to the entire folder path leading to the folder where the data are stored. Consequently, you will not be able to use nirsLAB to process data stored in, for example, a 'My Documents' folder.

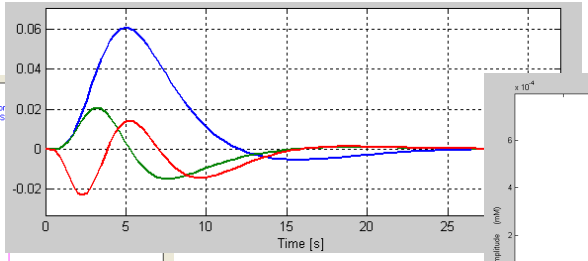
Normally, *filename*.wl1 contains data for the 760 nm measurement wavelength, while *filename*.wl2 holds the data for the 850 nm (NIRScout or NIRSport) or 830 nm (DYNOT) wavelength. The *filename*.set file records the gain settings assigned to all measurement channels by the imaging system, based on the detected signal strengths. The *filename*.evt file contains user-recorded information associated with the measurement protocol (*e.g.*, starting and/or ending times for different experimental conditions). The *filename*_config.txt file contains information regarding the experimental configuration (*e.g.*, number of laser diodes, numbers of sources and detectors, data sampling rate). The data formats of all the files are described in detail in the user's manual for each type of NIRx imager system.

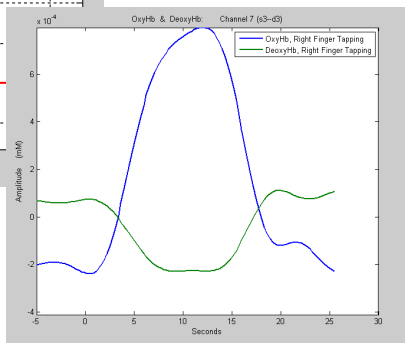
5.2 Probe Setup

As mentioned in Section 4.2.4, nirsLAB provides functions for topographically mapping the hemodynamic states onto head and brain surfaces. Before these capabilities can be used, nirsLAB needs to know the anatomical locations of the optodes on the subject's scalp, and which pairings of source and detector constitute experimentally relevant channels. As indicated in Section 4.2.6, this information is communicated to nirsLAB either by loading a probeInfo file generated during a previous session, or by using the *Setup probes* tool in the *Utilities* portal. One method or the other must be used to supply probe-setup information to nirsLAB before you will be able to preprocess your measurement data.

nirsLAB





Chapter 2:Experimental Data and Conditions

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1 Introduction

The components in the **Experimental Data and Conditions portal**, shown in Figure 2-1, are used to load data sets produced by a NIRx imaging system (NIRScout, NIRSport or DYNOT) and initialize a nirsLAB project, load a probeInfo file previously generated with the **Setup probes** utility (Chap. 7), load and (if necessary) edit a previously generated event-records file, or create an event file in cases where one does not already exist.

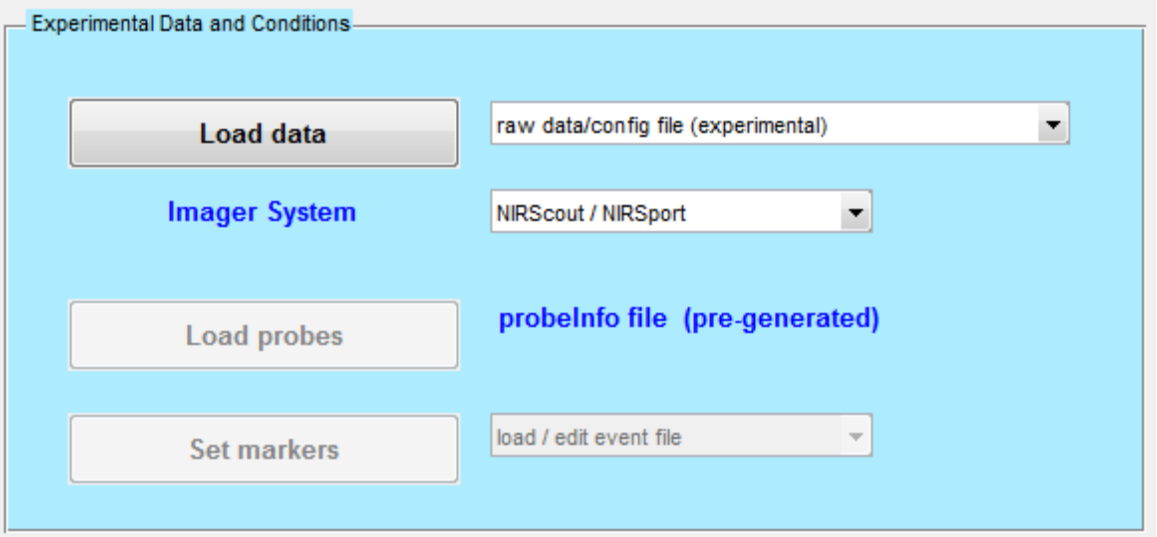


Figure 2-1. *Experimental Data and Conditions* portal, as it appears at nirsLAB startup.

Components consist of:

- *Load data* button.
- Pull-down menu for specifying file type to load (_config.txt or nirsInfo file).

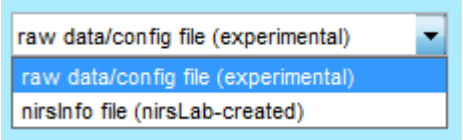


Figure 2-2. File-type pull-down menu.

- Pull-down menu for specifying imager type (NIRScout/NIRSport, or DYNOT).

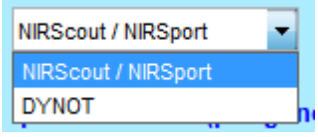


Figure 2-3. Imager-type pull-down menu.

- *Load probes* button (disabled until a _config.txt or nirsInfo file is loaded).

- *Set markers* button (disabled until a _config.txt or nirsInfo file is loaded).
- Pull-down menu for specifying whether to load an existing events-record file, or create a new one (disabled until a _config.txt or nirsInfo file is loaded), Figure 2-4.

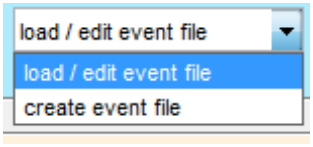


Figure 2-4. Event-file pull-down menu.

2 Loading Raw Data

Take the following steps to load a data set and initiate a project in nirsLAB:

1. Launch nirsLAB as described in Chap. 1, Section 3.
2. From the *Imager System* pull-down menu (Figure 2-1, Figure 2-3), select the type of imager that was used for data collection. The *NIRScout / NIRSport* menu item is the default option.
3. Specify the type of data to be loaded. If the data set you wish to process has not previously been loaded into nirsLAB, or if you want to overwrite all results obtained in earlier processing sessions, then select the 'raw data/config file (experimental)' default option from the pull-down menu next to the *Load data* button (Figure 2-1, Figure 2-2). (Otherwise, skip to Step 5.)
4. Click on the *Load data* button to open a browser window (Figure 2-5), which is used to navigate to the folder where the files produced by the imager system (Chap. 1, Section 5.1) are stored. We refer to this as the "project-root folder." Select the file whose name ends in '_config.txt' from the folder. Click on the *Open* button, and nirsLAB will automatically load the data and to initiate the project (*i.e.*, will create a nirsInfo file).

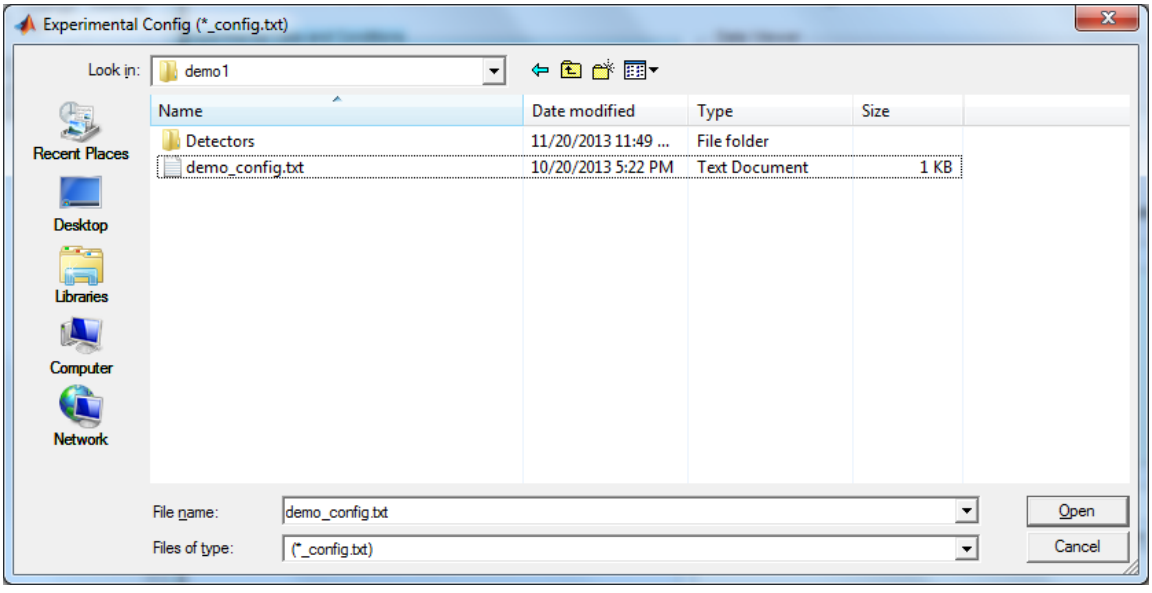


Figure 2-5. Browser window

During the project-initiation process, a progress-bar window will automatically pop up on your screen (Figure 2-6), and it will automatically close when the process is complete.

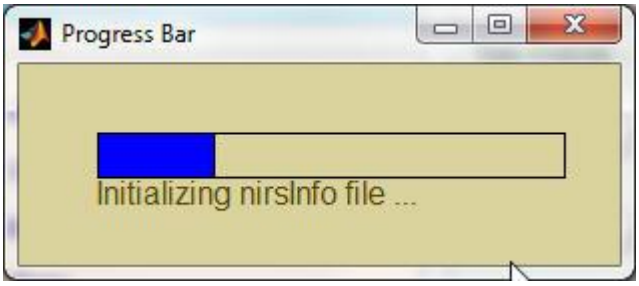


Figure 2-6. Progress-bar window that pops open when the *Open* button shown in the lower right corner of Figure 2-5 is pressed.

After the nirsLAB project has been initiated, you will be able to see that the project-root folder contains a new MATLAB binary file with the name *filename*_nirsInfo.mat, where, as explained in Chap. 1, Section 5.1, *filename* is the name applied to all of the files that were generated by the imager when the measurement was performed.

The project-root folder also will contain a new sub-folder, named *Detectors*. In it you will find a file named *filename*b.dat. This file contains an exact copy of the contents of the *filename*.wl1 and *filename*.wl2 files, combined into a single file that has a binary format.

The nirsInfo file acts as an electronic ledger and is unique for a specific nirsLAB project. An important role that the nirsInfo file plays is that after project initialization, it becomes the only file you will need to load in subsequent nirsLAB sessions if you want to review results or to perform additional processing steps. Also, as data processing proceeds the nirsInfo file is continually updated to maintain a record of every analysis operation that has been performed and every parameter setting that has been specified.

5. If a nirsInfo file already exists and you do not want to overwrite the results generated in previous nirsLAB sessions, select the 'nirsInfo file (nirsLAB-created)' item from the pull-down menu depicted in Figure 2-2. Then click on the *Load data* button (Figure 2-1), use the pop-up browser (Figure 2-5) to navigate to the folder containing the nirsInfo file, highlight that file to select it, and click on the *Open* button. nirsLAB will automatically load the information it needs to permit further processing or review of previously generated results.

6. If the project-root folder already contains a nirsInfo file, nirsLAB still allows you to click on the *Load data* button with the default 'raw data/config file (experimental)' option selected in the pull-down menu depicted in Figure 2-2. However, in this situation nirsLAB must distinguish between the following possibilities:

    a. You wish to restart the data processing sequence "from scratch" and to overwrite the existing nirsInfo file with a new one.

b. You do not wish to overwrite the existing nirsInfo file, and you have inadvertently clicked on the *Load data* button with the incorrect menu option selected.

In order to decide which of the preceding possibilities is correct, nirsLAB will open the following pop-up window after you select a '_config.txt' file.

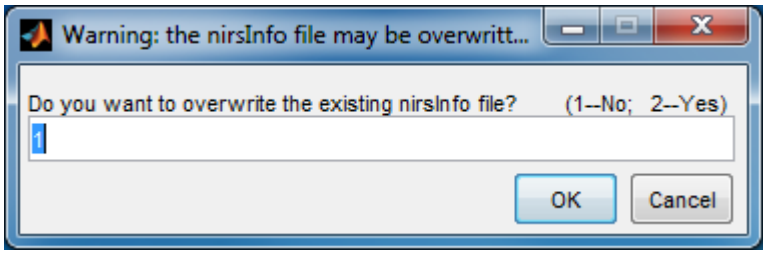


Figure 2-7. Pop-up window that opens if the *Load data* button (Figure 2-1) is pressed with 'raw data/config file (experimental)' selected from the drop-down menu depicted in Figure 2-2, but the project-root folder already contains a nirsInfo file.

If you really do want to create a new nirsInfo file and to replace all of the processing results that were previously generated, then change the default value of '1' in the number field to '2' (*i.e.*, '1' = 'no', '2' = 'yes'), and click on the *OK* button depicted in Figure 2-7. The pop-up will close, and a new nirsInfo file will be generated as described in Step 4.

However, if you selected 'raw data/config file (experimental)' inadvertently, then simply click on the *OK* button depicted in Figure 2-7 without changing numerical value in the number field. The pop-up will close, and nirsLAB will open the following message window on your screen to remind you to select the 'nirsInfo file (nirsLAB-created)' item from the pull-down menu depicted in Figure 2-2. (The same will happen if you enter any number other than '2'. However, an error message will be written to the MATLAB command window if you enter non-numerical text.)

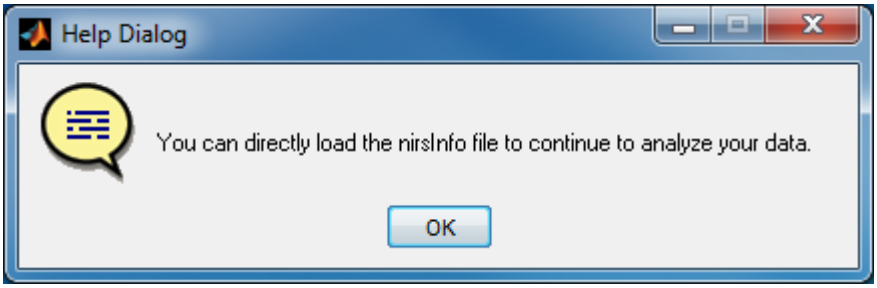


Figure 2-8. Pop-up window that opens if you click on the *OK* button seen in Figure 2-7 without changing the value in the number field to '2'.

3 Loading Probes

After a nirsInfo file is either loaded or created, it is necessary to load the probeInfo file that identifies the positions of the optodes used to collect the experimental data. Depending on how far you have gone in

the data-processing sequence before you reach this point, one of the following three courses of action will be appropriate for you:

a. If the relevant probeInfo file does not already exist, use the **Probe Setup** tool to generate one (see Chap. 7). After you complete the probe-setup operation, click on the *Load probes* button (Figure 2-1), which becomes enabled after a nirsInfo file is loaded or created, to open a browser window. Navigate to the folder where the probeInfo file is stored. Highlight the probeInfo file to select it, and click on the *Open* button to load the file.

b. If the relevant probeInfo file does exist but has not already been associated with the nirsInfo file, click on the *Load probes* button (Figure 2-1), which becomes enabled after a nirsInfo file is loaded or created, to open a browser window (Figure 2-5). Navigate to the folder where the probeInfo file is stored. Highlight the probeInfo file to select it, and click on the *Open* button to load the file.

c. If the relevant probeInfo file does exist and has already been associated with the nirsInfo file, no further action is necessary. You may proceed directly to Setting Markers.

4 Setting Markers

The set of output files generated by NIRx imagers include one called *filename*.evt, which is intended to record important temporal information relevant to a measurement (*e.g.*, starting times for presentation of stimuli). If you view the contents of this file with a text editor, you will see that it has the structure depicted in Figure 2-9, where the time (in units of frames, as described in Section 4.1) at which a marker

```
.
.
.
821   0     1     0     0     0     0     0     0
925   1     0     0     0     0     0     0     0
1029  0     1     0     0     0     0     0     0
1133  1     0     0     0     0     0     0     0
1237  0     1     0     0     0     0     0     0
.
.
.
```

Figure 2-9. A portion of an event-record (.evt) file generated by a NIRx imager.

was created is recorded in the first column of numbers, and event markers for the n^{th} user-defined event type are indicated by '1' s in the $(n + 1)^{th}$ column. (Note that these event identifiers actually correspond to 8-bit binary numbers generated by the imager. This provides for up to 255 non-zero values that can be identified with different events.)

In general, two methods are available for recording information in the *filename*.evt file: the user can manually enter markers using either the event-marker button on the NIRStar user interface or 'function'

keys on the keyboard (see NIRStar 13.0 User Manual); or event marker information can be transferred from a timestamp-generating device to the imager via a specially designed cable that you may obtain from NIRx. It is permissible for you to use both methods during a single measurement session. If you do not make any use of either method, the measurement-session output will still contain a *filename*.evt file, but it will be empty.

nirsLAB provides an editor that allows you to view and edit elements of the event record. If an imager-generated file is not available (*e.g.*, it is an empty file, as described in the preceding paragraph), the editor can be used to create one. If the event-record file exists but it is incomplete or not entirely accurate (*e.g.*, the user recorded some marker information in the incorrect column of the file, or did not press the event-marker button until sometime after the event actually occurred), the editor can be used to modify the existing event-record information.

Once the *Set markers* process has been carried out, all measurement-timing information will be incorporated into the nirsInfo file. Consequently, if you load the same nirsInfo file in a later nirsLAB session, you will not have to repeat the process of loading or creating an event file.

The procedure for creating or editing the experimental-event information and attaching it to the nirsLAB project is:

1. Select an item from the pull-down menu shown in Figure 2-4. If you want to work with the event file generated by the imager, or to modify event-record information already incorporated into the nirsInfo file, select the default 'load / edit event file' item. If you don't have a non-empty event file for the measurement, or if for any reason you prefer not to use the imager-generated file, select the 'create event file' item. Then click on the *Set markers* button (Figure 2-1).

2. 'load / edit event file' menu item. If the project-root folder contains a file that has the filename extension '.evt' and the same filename as the '.wl1' and '.wl2' files (see Chap. 1, Section 5.1), it will automatically be loaded by nirsLAB. However, if the that folder either:

   - does not contain any file with the '.evt' extension, or
   - contains one or more files having the '.evt' extension, but they all have filenames different from the filename shared by the '.wl1', '.wl2',

   then a Help Dialog window will pop open on your monitor, containing the message "Please load an event file, or create new event file." A browser window will pop open at the same time. Use the browser to navigate to the folder containing the file you want to load, and to select it. After you have selected a file, the *Set markers* GUI will pop open. An example of what you will see is shown in Figure 2-10. Also, a Help Dialog window will pop open on your monitor, containing the message "Please specify Stimulus Duration first !"

3. 'create event file' menu item. The *Set markers* GUI will pop open. Also, a Help Dialog window will pop open on your monitor, containing the message "Please specify Stimulus Duration and Number of Conditions first !" The GUI for this case will look almost exactly the same as the one

shown in Figure 2-10. The only gross difference will be that you won't see any colored vertical lines overlaid on the time-series plot. Those lines, when present, are a graphical depiction of the information that nirsLAB finds in the event file.

The subsequent steps in using the GUI are nearly the same for both the 'load / edit event file' and 'create event file' cases, so we will combine the descriptions for both of them.

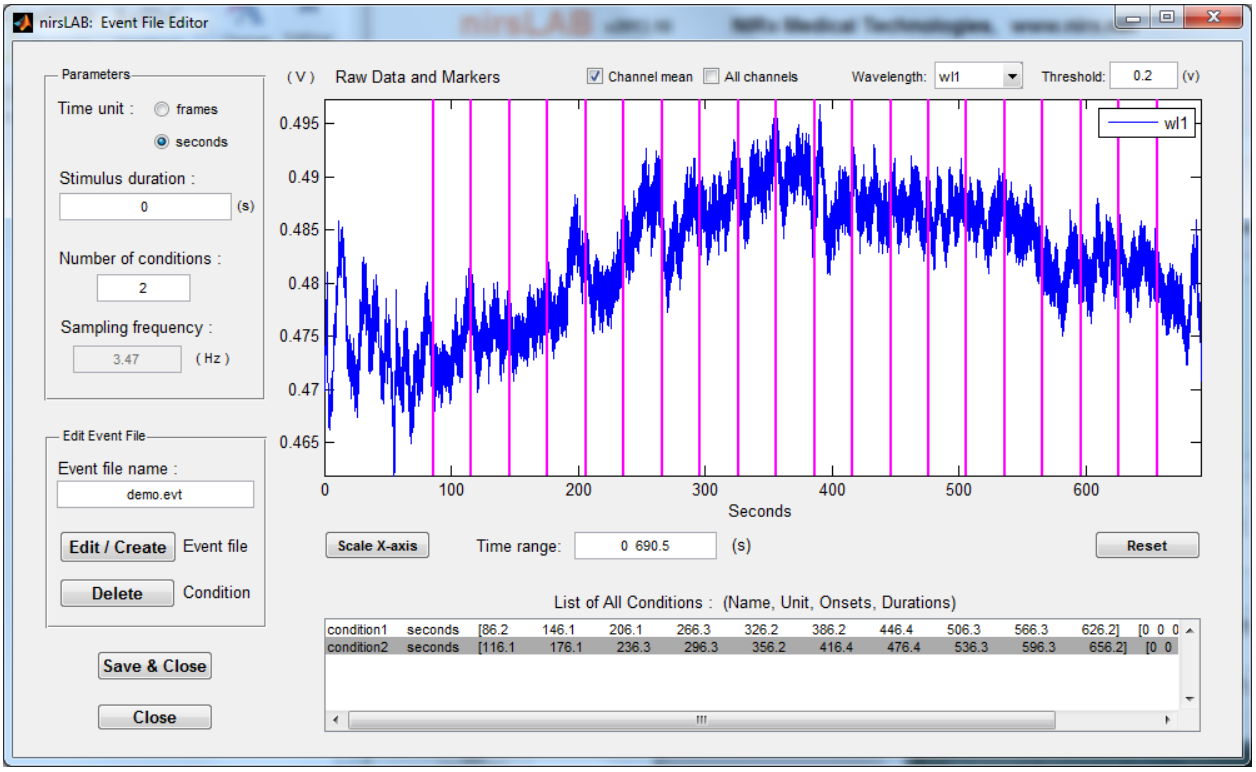


Figure 2-10. Set markers GUI for the 'load / edit event file' case. (The 'create event file' GUI is the same, except for the absence of colored vertical lines on the plot.)

4.1 'Parameters' module

In both the 'load / edit event file' and 'create event file' cases, the information that nirsLAB asks you to specify first is entered through the 'Parameters' module seen in the upper left portion of Figure 2-10, and shown enlarged in Figure 2-11. As shown, the default 'Time unit:' is 'seconds'. You may select 'frames' if you like, and may toggle between the units at will. Each time you select a different unit, the numbers on the x-axis of the plot window, and in the 'Time range:' field (Figure 2-10), will automatically update.

If a task (*e.g.*, finger tapping) was performed during the measurement session, or a stimulus (*e.g.*, flashing checkerboard visual stimulus) was applied, enter the duration for each task or stimulus episode in the 'Stimulus duration :' field. Note that:

- The time unit you use for the stimulus duration must match the one that you have selected. The unit that nirsLAB expects is shown in parentheses to the right of the 'Stimulus duration :' field [(f) = frames, (s) = seconds].
- If the measurement involved more than one task or stimulus episode, and they did not all have the same duration, then enter the duration that occurred most frequently during the session. You will have an opportunity to adjust the duration for any specific episode in a later step (see Section 4.3).
- If the experiment involved more than one condition, and they had different durations, you may enter more than one number in the 'Stimulus duration :' field. For *N* experimental conditions, type in *N* space-separated values. If you enter only a single number, nirsLAB will use it as the duration for all experimental conditions, no matter how many there are (but you still can modify selected ones later [see Section 4.3]).

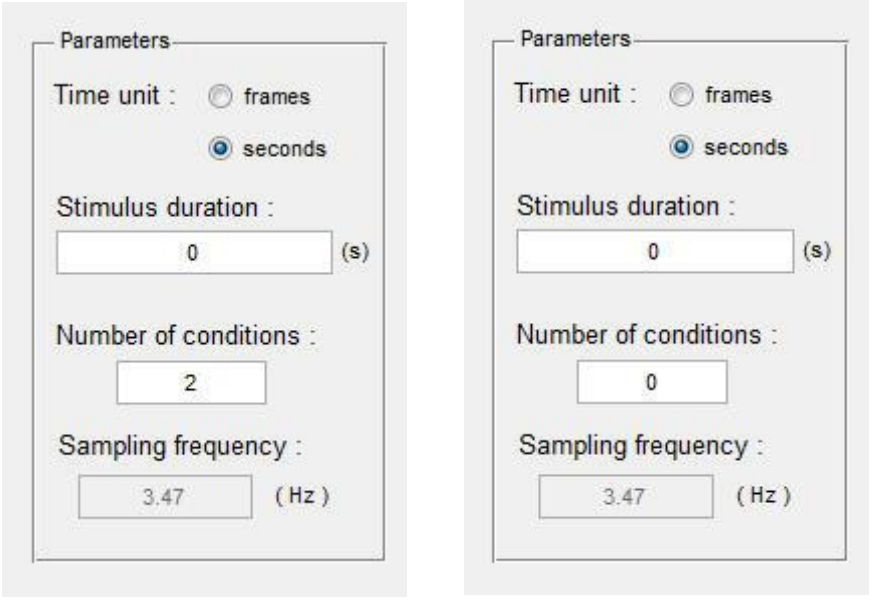


Figure 2-11. Enlarged view of the 'Parameters' module for the 'load / edit event file' (left) and 'create event file' (right) cases.

If you loaded an event file, the 'Number of conditions :' field will already display a value equal to the number of columns containing different bit values in that file. As seen in Figure 7, there are two columns containing event markers in the event file supplied with the sample data set, and so the *Set markers* GUI opens with a '2' already in the 'Number of conditions :' field. If you are creating an event file, there will be a '0' already in the 'Number of conditions :' field.

The numerical value in the 'Sampling frequency :' field is read directly from the configuration file (see Chap. 1, Section 5.1) by nirsLAB. It cannot be modified in the *Set markers* GUI. If you want to change the

displayed sampling frequency for any reason, you must edit the configuration file, change the number in the 'Samplingrate=' line there, and then generate a new nirsInfo file.

After you enter number of conditions and/or stimulus durations, press the 'Enter' key on the keyboard and they will take effect.

For the demo data set used for illustration, there are two experimental conditions (left-hand and right-hand finger tapping) and the duration for every task episode was 35 frames. The starting times for each episode (first column in Figure 2-9) are indicated by the colored vertical lines in the plot shown in Figure 2-10. nirsLAB obtained the starting-times information from the event file. The same file also contains the information that the tasks took places in a strictly alternating left-hand, right-hand manner (this is indicated by the pattern of 1s in the second and third columns in Figure 2-9). However, the stopping times for the task episodes are not included in the event file for this measurement. Consequently, nirsLAB assigns a default value of 0 for each task duration, as seen in the 'List of All Conditions :' box at the bottom of Figure 2-10, and enlarged in Figure 2-12. When we enter '35' in the 'Stimulus duration :' field and press the 'Enter' key, the task durations are updated as shown in Figure 2-12, and the time-series plot changes to the appearance shown in Figure 2-13.

Note that in the Figure 2-13 plot there is no explicit indication of which pairs of markers correspond to which experimental condition. However, simply clicking anywhere in the 'condition1' line in the 'List of All Conditions :' box will cause nirsLAB to highlight all the marker pairs associated with the first condition (left-hand tapping), and clicking anywhere in the 'condition2' line will cause it to highlight all the marker pairs associated with the second condition (right-hand tapping).

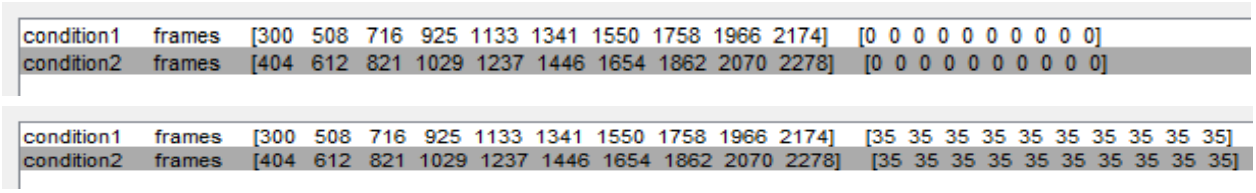


Figure 2-12. Contents of the 'List of All Conditions :' field before (top) and after (bottom) the correct value for the stimulus durations is entered in the 'Stimulus duration :' field.

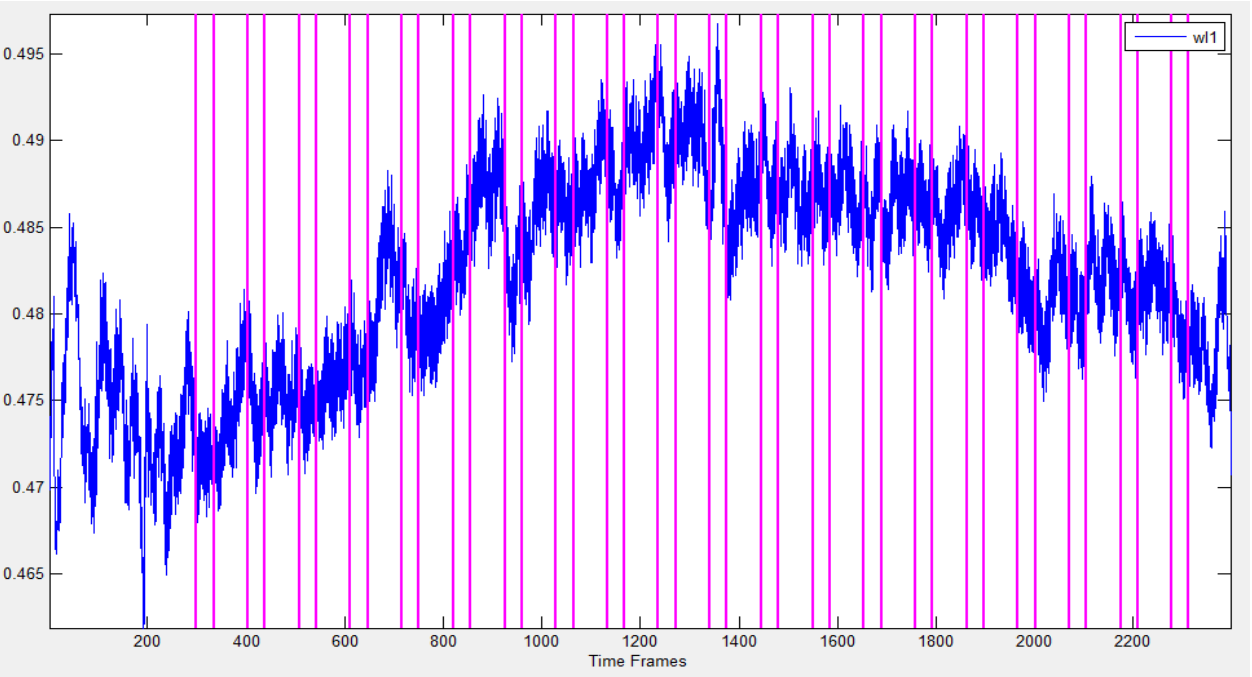


Figure 2-13. Time-series plot in the *Set markers* GUI changes to reflect the user-specified task durations.

4.2 Display Options

The default display options for the *Set markers* GUI, seen near the top of Figure 2-10, are shown enlarged in Figure2-14. Several options are available. For instance, the time series that is displayed by default, raw data for the first measurement wavelength, is the average amplitude over all channels that have raw-data values larger than a specified minimum threshold value (default value = 0.2 V). Use the pull-down menu if you want to display data for the second wavelength (the 'wl2' menu item), or for both at

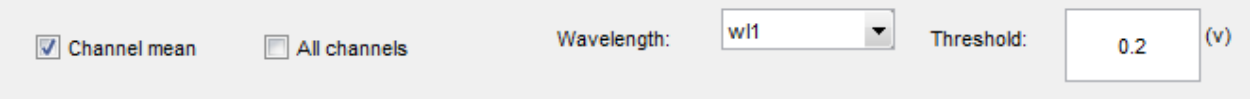


Figure 2-14. Default display options for the *Set markers* GUI.

the same time ('all'), instead of the first ('wl1'). In Figure 2-15 we show the channel-mean plot for the second wavelength, with the condition1 time intervals highlighted, and the channel-mean plot for both wavelengths together, with the condition2 time intervals highlighted and seconds chosen as the time unit. When you click in the 'All channels' checkbox, the channel-mean plot will be replaced by separate plots of the time series for all data channels, as shown in Figure 2-16. In this *Set markers* GUI, you will

not be able to directly determine which curve corresponds to which channel (that capability is available in other parts of nirsLAB, which are described in other chapters). However, you are afforded the ability to

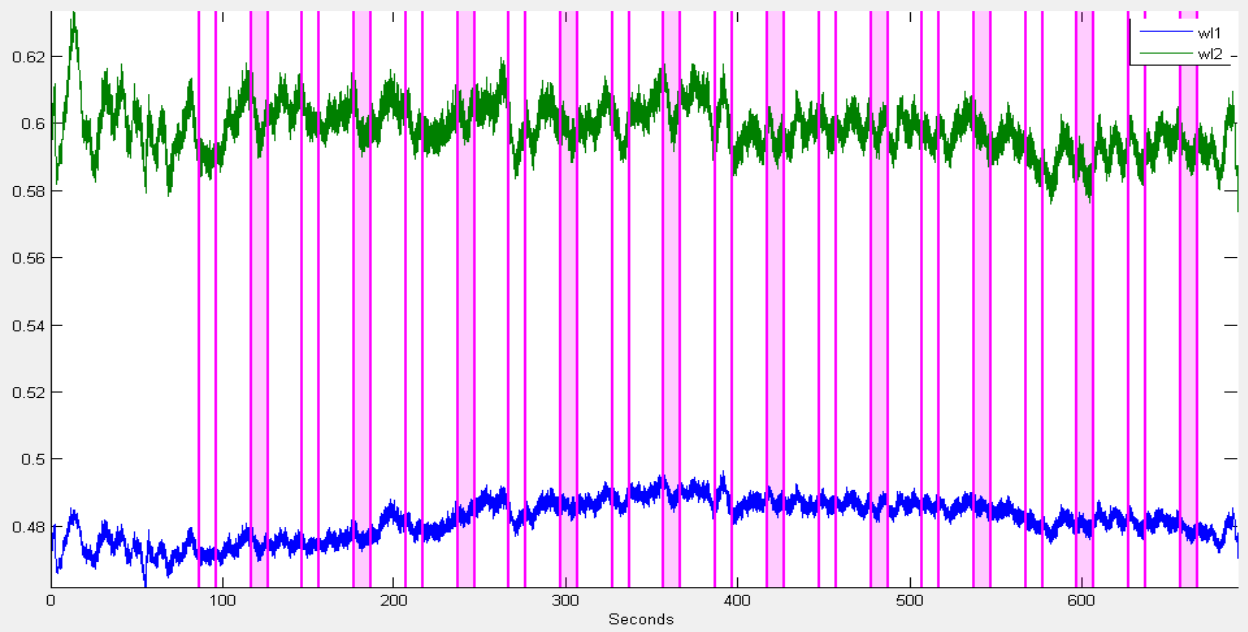


Figure 2-15. Display of channel mean for both wavelengths.

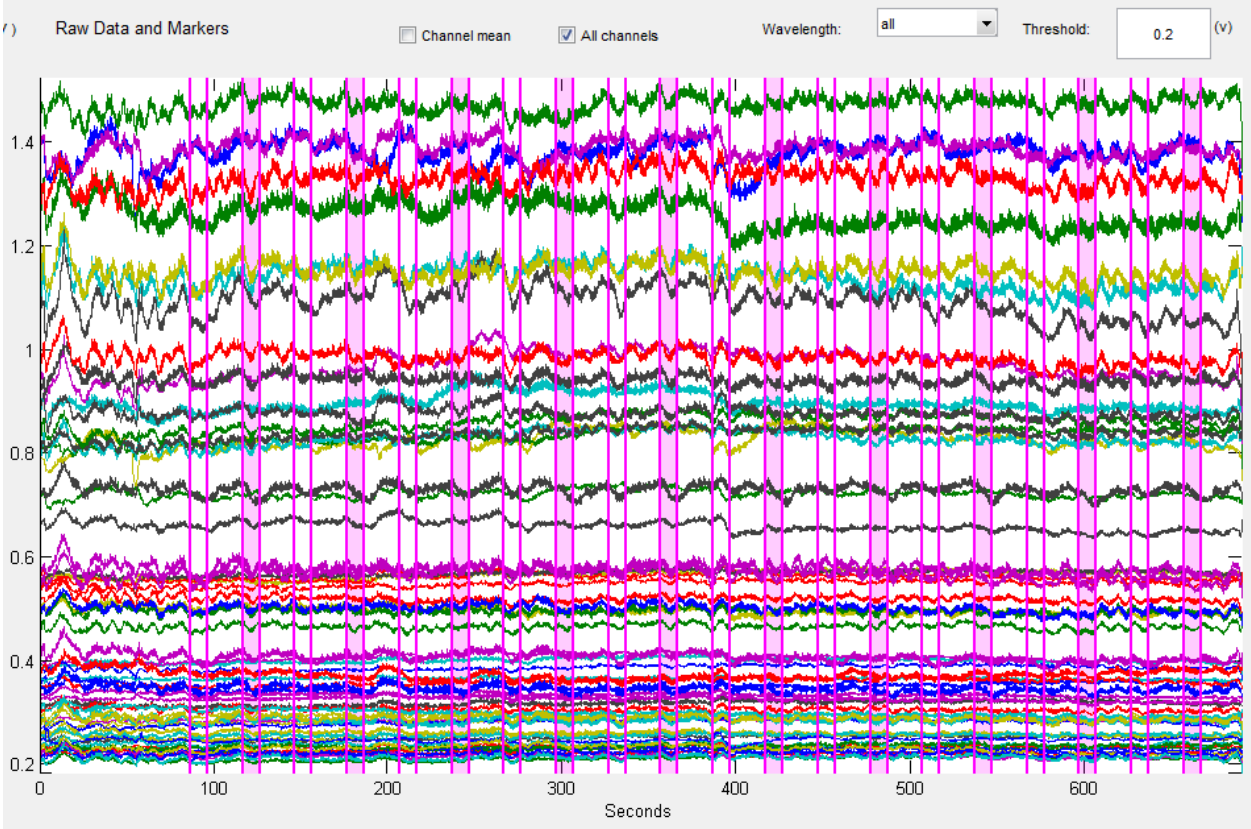


Figure 2-16. Separate time-series plots of raw data for all channels, at both wavelengths, with the default 0.2 V y-axis minimum.

adjust the lower limit of the y-axis range for the plot window, which is equal to the number in the 'Threshold:' field. You may type any number into the 'Threshold:' field. However, if the number you enter is so large that the plot will not include at least one channel for each wavelength, nirsLAB will automatically reduce the threshold to a value that allows at least one channel per wavelength to appear in the plot. (It will also automatically convert negative numbers to 0.) For example, for the demo data set used here, the largest threshold value that nirsLAB will accept is 0.91968 V, and any larger value is automatically reduced (see Figure 2-17).

Figure 2-17. A y-axis lower limit that does not allow at least one time series per wavelength to fit inside the plot window is automatically adjusted downward by nirsLAB.

By default, the full duration of the measurement (2397 frames ≈ 691 seconds, for the demo data set) is plotted on the x-axis of the plot window. You can zoom in on a smaller time interval in either of two ways. First, you can type the starting and ending times directly into the 'Time range:' field and press the 'Enter' key on your keyboard, as depicted in Figure 2-18. The plot will automatically update, as shown in Figure 2-19, revealing in this example that the high-frequency component seen in the Figure 2-13 plot is a highly regular oscillation (*i.e.*, it is the subject's cardiac rhythm).

Figure 2-18. Controls for adjusting the time interval displayed on the plot window x-axis. (Top) The default time interval is the full duration of measurement. (Bottom) the user can enter different numerical limits in the 'Time range:' field.

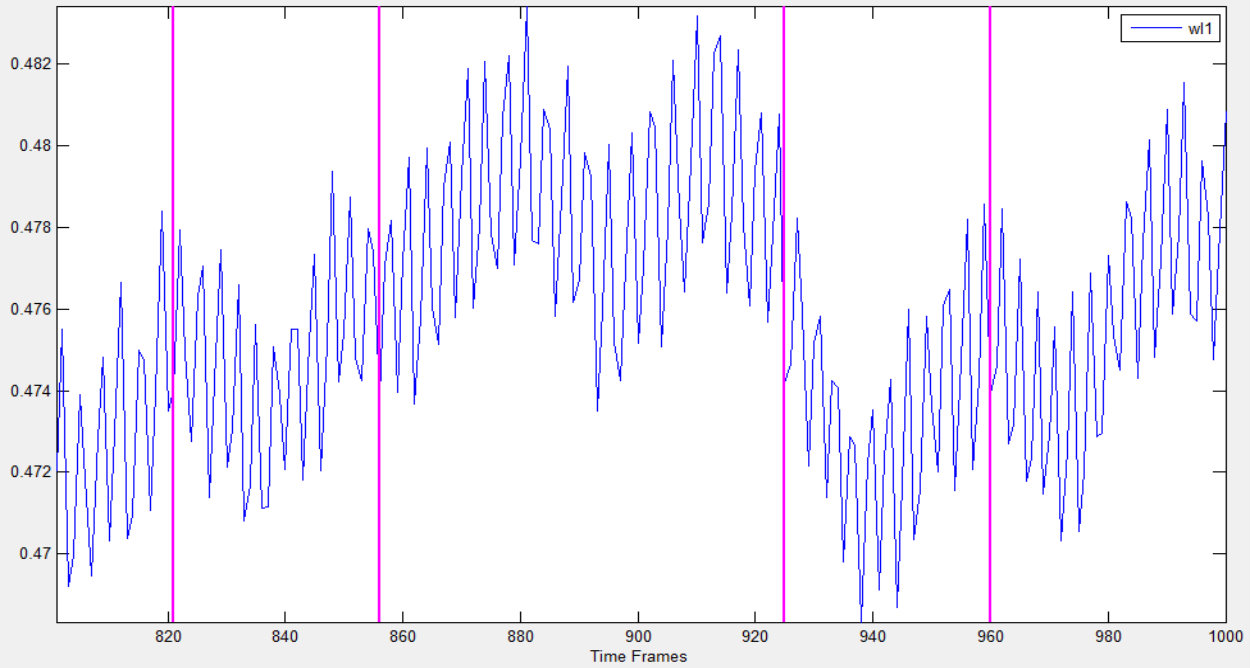


Figure 2-19. Detail from the same time-series that is plotted in Figure 2-13, after zooming in on the x-axis.

The second method for changing the displayed time-axis interval is to click on the *Scale X-axis* button also shown in Figure 2-18, which will activate a set of crosshairs. Place them in the plot window, with the vertical crosshair at the starting point of the time interval that you want to display, as depicted in Figure 2-20, and click with your mouse. Then place the vertical crosshair at the ending point of the time interval, and click a second time. The plot will automatically update upon the second click.

No matter which method you use to change the displayed time interval, you can restore the original view simply by clicking the *Reset* button shown in Figure 2-18.

Finally, note that the time series data displayed in the *Set markers* GUI correspond to all data collected and is not limited by the channels specified in by the probesinfo file. Thus, depending on the optode arrangement employed, it can be expected that at least some of the channels will be noise dominated.

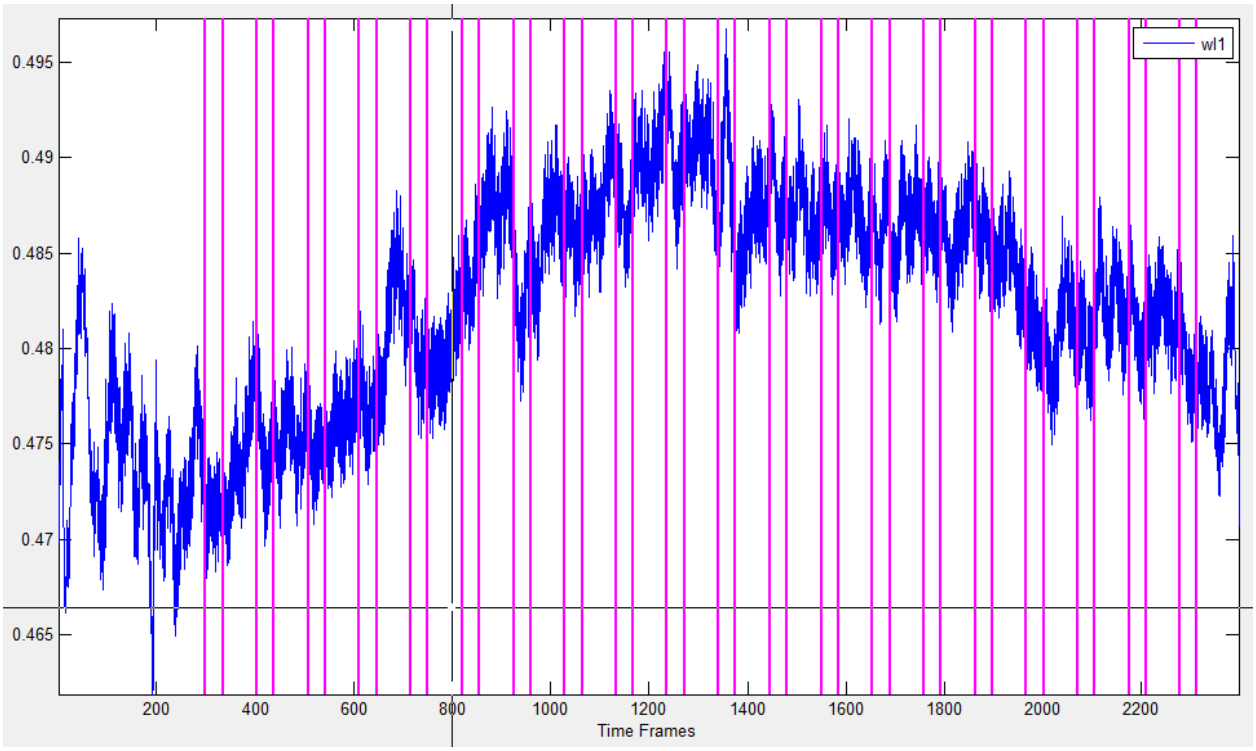


Figure 2-20. Use of the crosshairs to select the time interval to display on the x-axis, after clicking on the *Scale X-axis* button shown in Figure 2-18.

4.3 'Edit Event File' module

As shown in Figure 2-21, there will be a nirsLAB-supplied default filename in the 'Event file name :' field. If you are using the 'load / edit event file' option, it will be the name of the event file that you loaded. If you are using the 'create event file' option, the suggested filename will match the filename prefix of the nirsInfo file. You have the option of specifying a different name for the new event file that nirsLAB will generate after you have completed the editing (or creation) process (see Section 4.4).

If you want to modify the experimental conditions information in any way (*e.g.,* because the task or stimulus episodes did not all have the same duration, or because there is an experimental condition in addition to the ones recorded in the event file), click on the *Edit / Create* button. This will cause the pop-up window shown in Figure 2-21 to open on your monitor. You can modify the condition name in the first field (*e.g.*, for the demo data set considered here, we might want to call them 'LeftHand' and 'RightHand' instead of the default 'condition1' and 'condition2'), or the onset times (*i.e.*, start times for the task or stimulus episodes) in the second, or the episode durations in the third. If there is more than one condition, then the pop-up window will automatically refresh to show the corresponding information for the next one when you click on the *OK* button. The window will close when you click on *OK* after editing the information for the last condition.

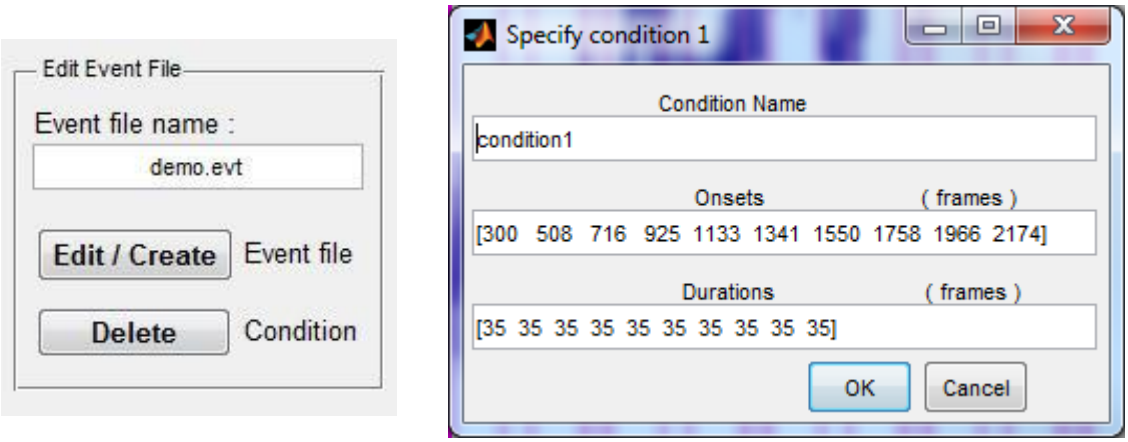


Figure 2-21. (Left) Enlarged view of the 'Edit Event File' module. (Right) Example of the pop-up window that opens when the *Edit / Create* button is clicked.

When you modify the conditions information, there is a risk that you may inadvertently end up with different numbers of values in the 'Onsets' and 'Durations' field. If this happens, a pop-up window will open on your monitor, containing the message "The number of onsets is different from the number of durations! Please check it."

In some cases you may wish to remove an experimental condition that was recorded in the event file (*e.g.*, because a 'function' key on the keyboard was accidentally pressed during the measurement session, or a condition that records times when there was excessive subject motion). To do so, highlight a condition that you want to eliminate, by clicking on the corresponding line in the 'List of All Conditions :' window (see Figure 2-12). Then click on the *Delete* button shown in Figure 2-21. Note, the deletion of a selected event does not alter the primary data in any way. It will, however, affect subsequent computations such as a block average or SPM computations.

4.4 Saving changes and Exiting

To finalize the event information that you have modified or created, and add it to the nirsLAB project, click on the *Save & Close* button in the lower left corner of the *Set markers* GUI (see Figure 2-10). The GUI will close, and you will find that there is a new sub-folder in the project-root folder, named *Conditions*. In it you will find two files: a text file named *filename*.ext and a MATLAB binary-format file named *filename*_cond.dat. Here, the *filename* prefix is either the name that was in the 'Event file name :' field (see Figure 2-21) when you clicked on the *Save & Close* button, whether it is the nirsLAB-supplied default name or one that you specified. The *filename*_cond.dat file contains the time unit, condition name, onset times and durations that you specified, in a MATLAB structure array.

If, for any reason, you want to exit without saving any changes, click on the *Close* button in the lower left corner of the *Set markers* GUI (see Figure 2-10).

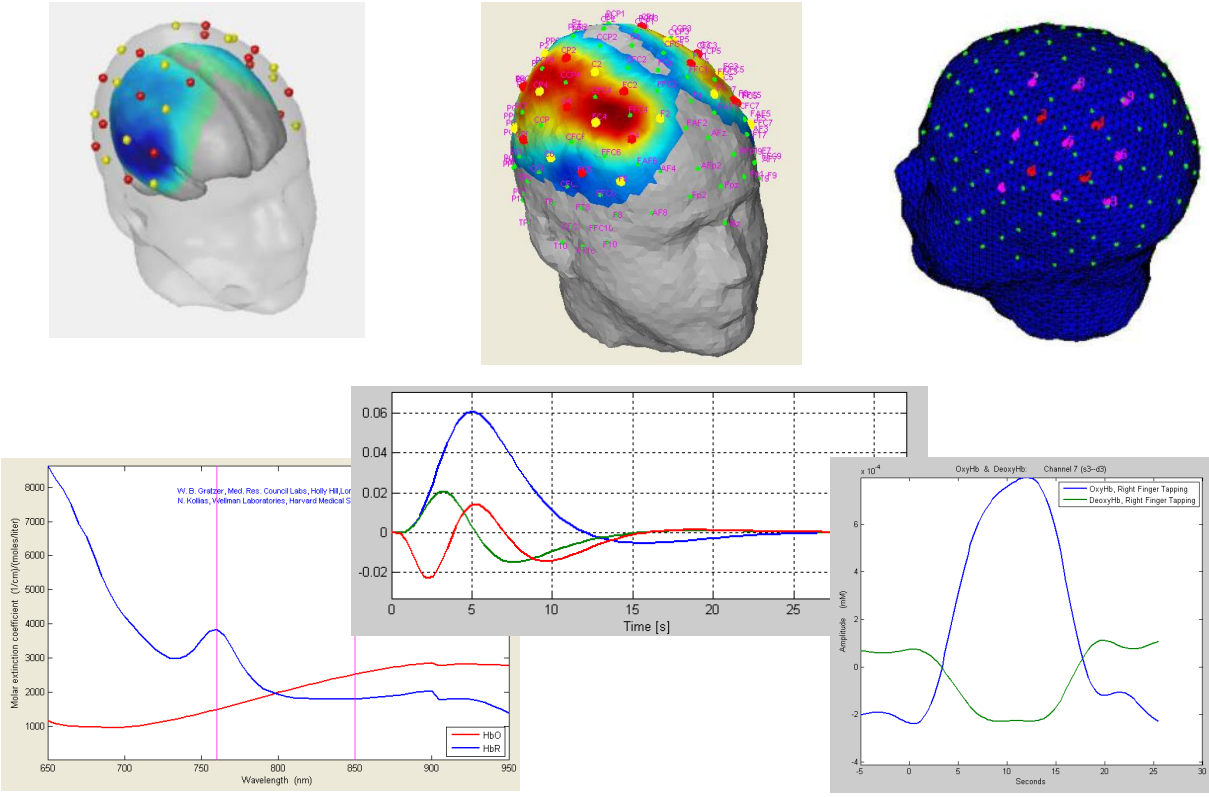
4.5 New Files Created

Processing of data using the 'Experimental Data and Conditions' portal generates three types of saved data files;

- *filename*_nirsInfo.mat
- A Conditions folder containing the *filename*.evt and *filename*_cond.dat files
- A Detectors folder containing the *filename*b.dat.

These files/folders are updated depending on the selected subsequent processing steps available in nirsLAB.

nirsLAB



Chapter 3: Data Preprocessing

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1 Introduction

The components of the *Data Preprocessing* portal, shown in Figure 3-1, are used to delete experimentally irrelevant time intervals from data, remove artifacts ("steps" and "spikes") from data, and apply band-, low- or high-pass frequency filters to exclude experimentally irrelevant frequency bands. Note that all buttons in the 'Data Preprocessing' module are grayed out at nirsLAB startup, as shown in Chap. 1, Figure 1-1. They become enabled after you complete the steps, described in Chap. 2, of adding measurement data, probe position information, and experimental timing information to the project-specific nirsInfo file.

Figure 3-1. *Data Preprocessing* portal, as it appears after the user has completed all required operations in the *Experimental Data and Conditions* portal (Chap. 2).

Components include:

- *Check raw data* button — launches the GUI used to evaluate the raw-data signal quality for the measurement channels defined in the probeInfo file previously generated with the **Setup probes** utility (Chap. 7)
- *Truncate Time series* button — launches the GUI used to exclude selected time intervals from further consideration.
- *Remove Discontinuities* button — launches the GUI used to remove discontinuous shifts in measurement values (*i.e.*, "step" artifacts) from data time series.
- *Remove Spike Artifacts* button — launches the GUI used to remove brief fluctuations (*i.e.*, "spike" artifacts) from data time series.
- *Apply Frequency filter* button — launches the GUI used to apply band-pass, low-pass or high-pass frequency filters to time-series data.

An important design feature of nirsLAB is that results of the data preprocessing operations described in this chapter are not saved as user-accessible output files (unless you make a point of creating such

files, by using the *Data export* utility described in Chap. 8). For frequency filtering, which is the most computation-intensive of the preprocessing operations, nirsLAB generates an output file named f_*filename*.dat, having a binary format (*i.e.*, you cannot directly view or edit this file), in the *Detectors* sub-folder. For the other preprocessing operations, nirsLAB saves instructions for performing the preprocessing operations, in the project-specific nirsInfo file, and performs them "on the fly" whenever they are needed in subsequent data-processing steps. This has the effect of reducing the amount of disk space required for a project. Since these other preprocessing operations have small computational burdens, you should not notice any tradeoff in terms of decreased processing speed.

1 *Check raw data* GUI

Click on the *Check raw data* button to launch the *Raw Data Checking* GUI depicted in Figure 3-2. As

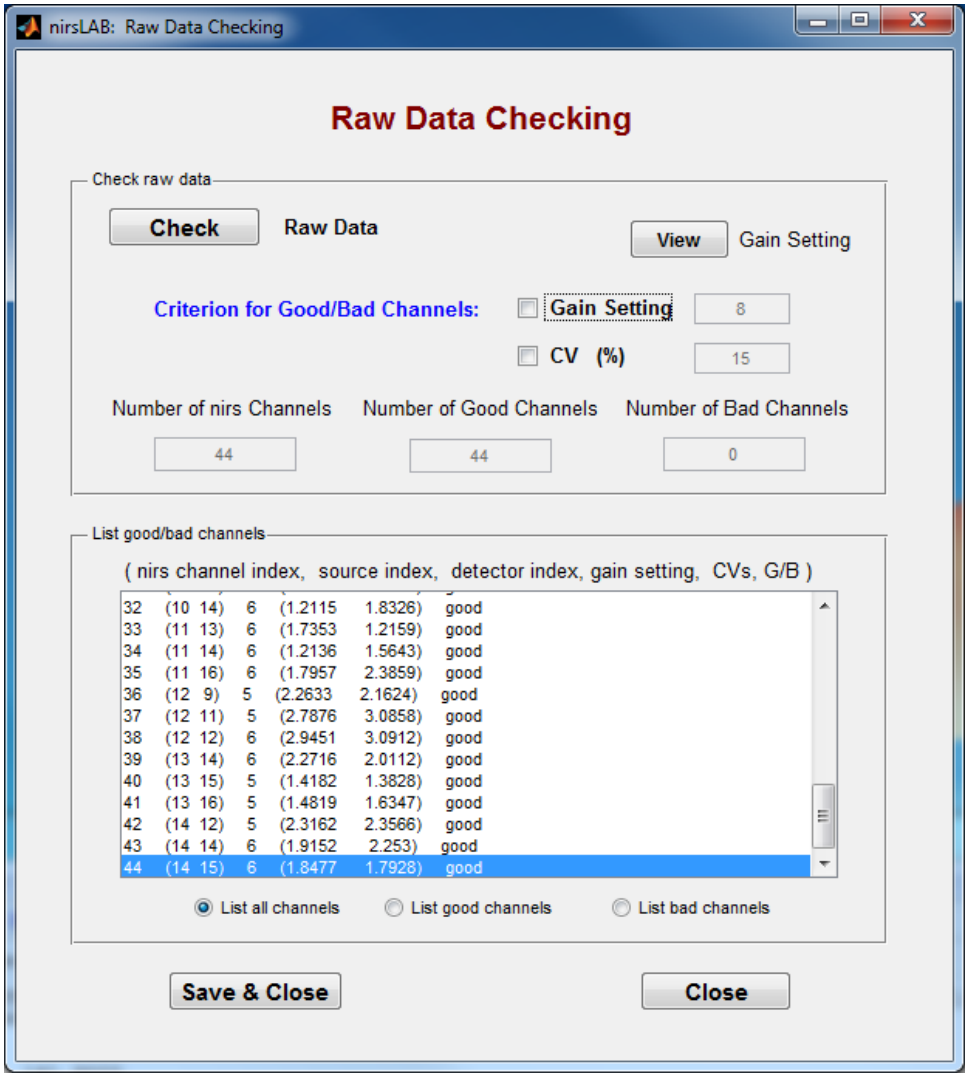

nirsLAB: Raw Data Checking
Raw Data Checking
Check raw data
Check
Raw Data
View
Gain Setting
Criterion for Good/Bad Channels:
Gain Setting
8
CV (%)
15
Number of nirs Channels
Number of Good Channels
Number of Bad Channels
44
44
0
List good/bad channels
(nirs channel index, source index, detector index, gain setting, CVs, G/B)
32 (10 14) 6 (1.2115 1.8326) good
33 (11 13) 6 (1.7353 1.2159) good
34 (11 14) 6 (1.2136 1.5643) good
35 (11 16) 6 (1.7957 2.3859) good
36 (12 9) 5 (2.2633 2.1624) good
37 (12 11) 5 (2.7876 3.0858) good
38 (12 12) 6 (2.9451 3.0912) good
39 (13 14) 6 (2.2716 2.0112) good
40 (13 15) 5 (1.4182 1.3828) good
41 (13 16) 5 (1.4819 1.6347) good
42 (14 12) 5 (2.3162 2.3566) good
43 (14 14) 6 (1.9152 2.253) good
44 (14 15) 6 (1.8477 1.7928) good
List all channels
List good channels
List bad channels
Save & Close
Close

Figure 3-2. *Raw Data Checking* GUI, as it appears upon being launched by pressing the *Check raw data* button seen in Figure 3-1.

shown, by default the 'List all channels' option is selected. Consequently, the large text window in the 'List good/bad channels' module contains a row of information for every channel that is defined in the probeInfo file. By way of illustration, the row that is highlighted in Figure 3-2 is:

```
44   (14 15)   6   (1.8477   1.7928)   good
```

- The first number, 44, is the scalar channel index. The channels are numbered 1 through *N* (with *N* = 44 for the demo data set), in the order in which you specify them when you generate the probeInfo file (Chap. 7).
- The ordered pair (14 15) indicates that the 14th source optode and 15th detector optode constitute the 44th measurement channel.
- The number 6 is the electronic gain factor that was applied to the received light. As explained more fully in the NIRStar User Manual, the larger the value for this factor, the more the photocurrent produced by the light signal is amplified. As a rule, the signal-to-noise ratio of data decreases as the gain factor increases. Consequently, nirsLAB allows you to identify the channels that have gain factors higher than a value that you select, and exclude them from consideration in the subsequent processing and analysis steps.

  If you click on the *View Gain Setting* button in the 'Check raw data' module (Figure 3-2), nirsLAB will generate a graphical display of the gain factors for all channels, as shown in Figure 3-3.

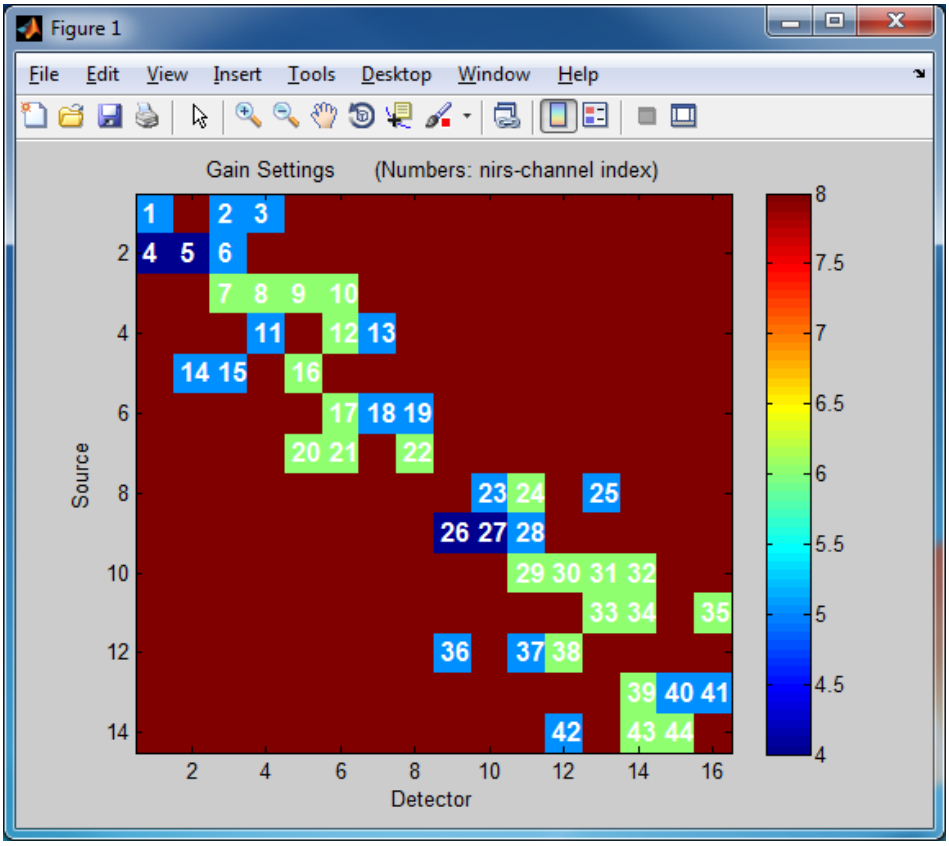


Figure 3-3. Example of a gain settings table, generated by clicking on the *View Gain Setting* button shown in Figure 3-2.

The scalar channel index is indicated by a white number overlaid onto one of the small colored squares, and the location of the square indicates which pairing of source (row) and detector (column) optodes defines that channel. The gain factor for each channel is indicated by the color of the corresponding square. Squares that do not have white numbers overlaid are combinations of source and detector that are not defined as measurement channels in the probeInfo file.

- The ordered pair (1.8477 1.7928) are the values of a metric that we use to quantify the signal-to-noise ratio of the raw data. The metric is called the coefficient of variation (CV). Two CV values are reported because there are two measurement wavelengths, and nirsLAB computes a CV for each one. The mathematical definition for a CV is 100 times the standard deviation divided by the mean value, where the standard deviation and mean are computed from all of the raw-data values in the measurement time series. If you click on the row of information that is highlighted in the 'List good/bad channels' module (Figure 3-2), nirsLAB will generate a graphical display of the raw data for both wavelengths, as shown in Figure 3-4. (For now, we will ignore the second

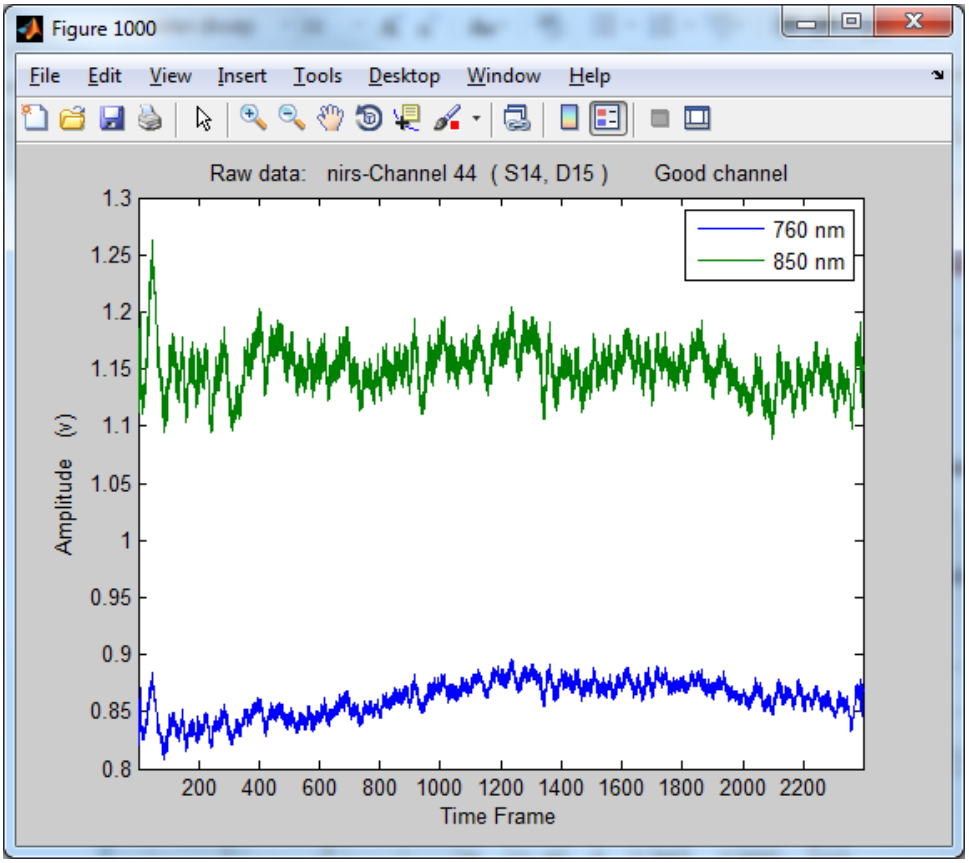


Figure 3-4. Example of a raw-data plot, generated by clicking on the highlighted row of information in Figure 3-2.

window that pops up with it—you can simply click on the *Cancel* button in its lower right corner to close it. Its function will be described at the end of this section.) Inspection of the plotted raw-

data time series can help you to understand why the CV is a metric of the data signal-to-noise ratio. You can see that the fNIRS signal fluctuates over time, but that the magnitude of the fluctuation (which is proportional to the standard deviation) is small in comparison to the average or mean value. Consequently, the CVs are small. However, if the data had a high noise level, or a substantial long-term drift, or discontinuities resulting from poor skin-optode contact, then the standard deviation, and hence the CV, would be significantly greater than the values that are seen in this example.

- The label 'good' in the final position is the status that nirsLAB currently has assigned to this channel. When you map hemodynamic-states data (Chap. 5) or perform data analysis (Chap. 6), nirsLAB will exclude data from any channels that, through any of the mechanisms that we describe next, become labeled as 'bad'.

An enlarged view of the 'Check raw data' module of the *Raw Data Checking* GUI is shown in Figure 3-5. You can see that, by default, neither the 'Gain Setting' box nor the 'CV (%)' box is checked. Consequently, the no channels are labeled as bad ('Number of Bad Channels' field), and the number of good channels ('Number of Good Channels' field) is equal to the total number ('Number of nirs Channels' field).

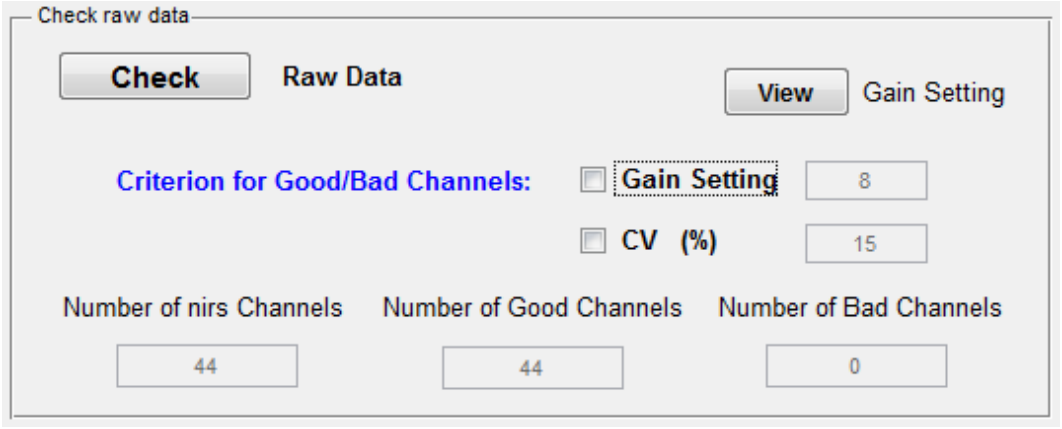


Figure 3-5. Enlarged view of the 'Check raw data' module of the *Raw Data Checking* GUI.

Checking the 'Gain Setting' box allows you to exclude all channels that have gain settings higher than a value that you will specify. (The previously described tendency for signal-to-noise ratio to fall with increasing gain value is the reason why you might want to do this.) As an example, we will lower the gain-setting threshold from 8 to 6, and then click on the *Check Raw Data* button seen in Figure 3-5. The appearance of the 'Check raw data' module changes as indicated in Figure 3-6. Half of the channels are now designated as 'bad'. The corresponding changes in the 'List good/bad channels' module is shown in Figure 3-7, where it is seen that channels having gain settings lower than the selected threshold still are labeled 'good', while channels with gain settings at or above the threshold are labeled 'bad'. We also can obtain a listing of only the channels designated 'good' by clicking the 'List good channels' radio button,

or of only the channels designated 'bad' by clicking the 'List bad channels' radio button. These options are illustrated in Figure 3-8, respectively.

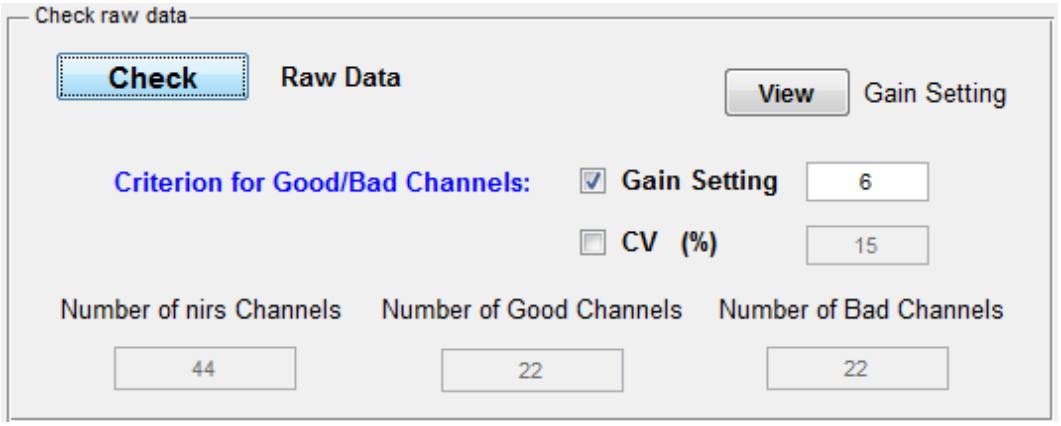


Figure 3-6. The result of running *Check Raw Data* with the 'Gain Setting' threshold set to 6.

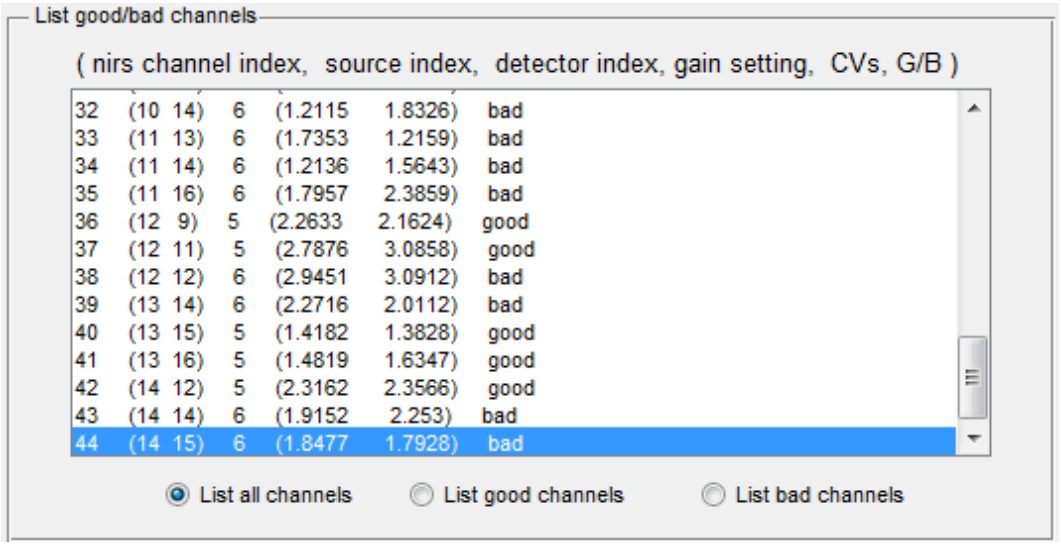


Figure 3-7. The result of running *Check Raw Data* with the 'Gain Setting' threshold set to 6.

By placing the checkmark in the 'CV (%)' box instead of the 'Gain Setting' box, you can likewise instruct nirsLAB to label as 'bad' any channel that has a CV, at either wavelength, equal to or greater than the threshold value that you specify in the 'CV (%)' number field. You also have the option of checking both boxes, thereby establishing a composite data-quality criterion: any channel that has either a too-high gain setting or a too-high CV is labeled a 'bad' channel.

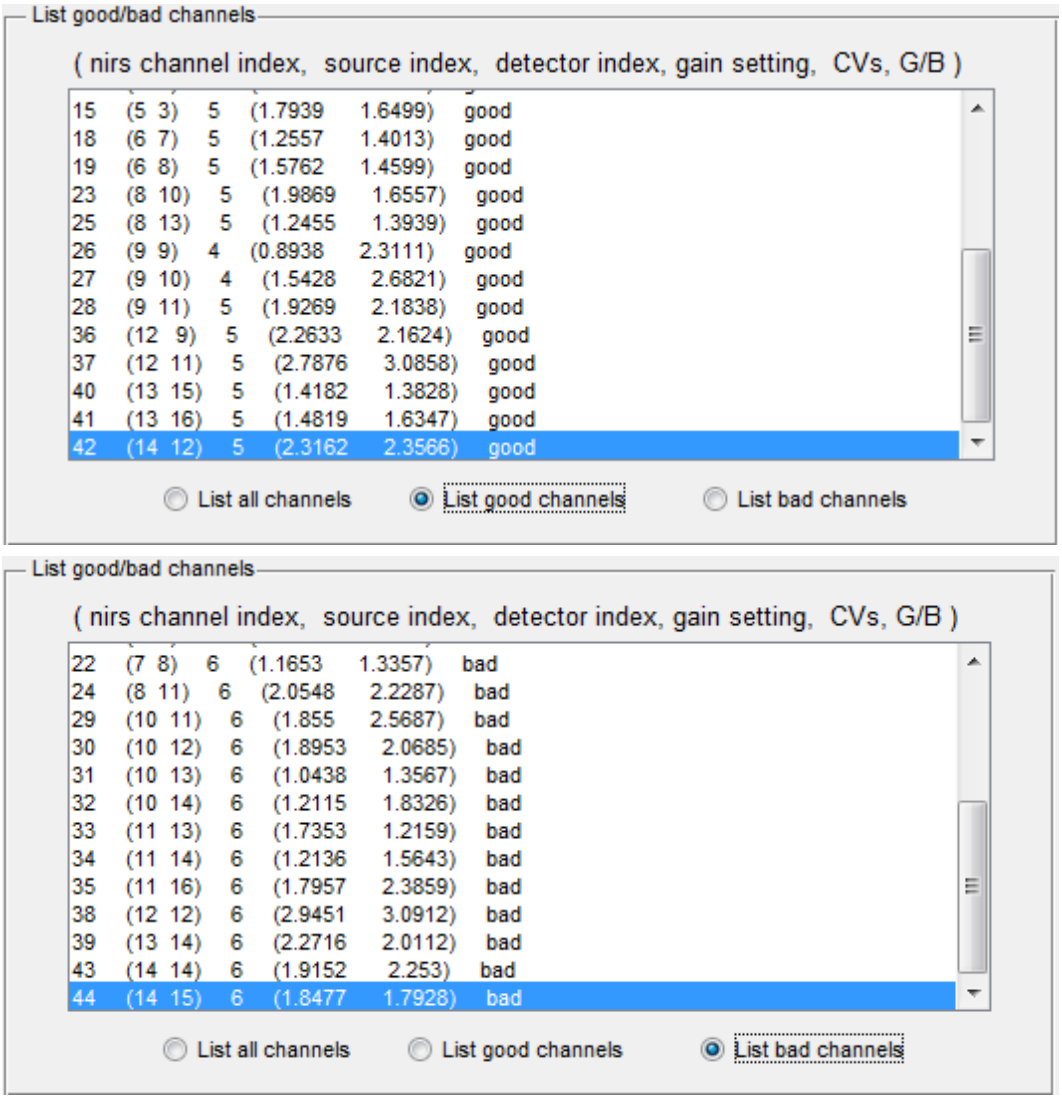


Figure 3-8. With the 'List good channels' option selected (top), only channels that satisfy the selected data quality criteria are displayed. With 'List bad channels' selected (bottom), only channels that fail to satisfy the selected data quality criteria are displayed.

In addition, nirsLAB allows you to make perform data-editing on the individual channels one at a time. This is the function of the previously mentioned second pop-up window that opens on your screen when you display the raw data time series for a selected channel (Figure 3-4). As shown in Figure 3-9, the second pop-up contains a number field in which you indicate whether or not you want to change the current status of the selected channel. In the illustrated example, the channel currently is included (*i.e.*, its status is 'good') and nirsLAB is asking if you want to exclude it (*i.e.*, to change its status to 'bad'). If you do, then change the default value of '1' in the number field to '2' (*i.e.*, '1' = 'no', '2' = 'yes'), and click on the *OK* button. Otherwise, simply click on the *OK* button without changing numerical value in the text field. The pop-up window will close, and your selection will be implemented.

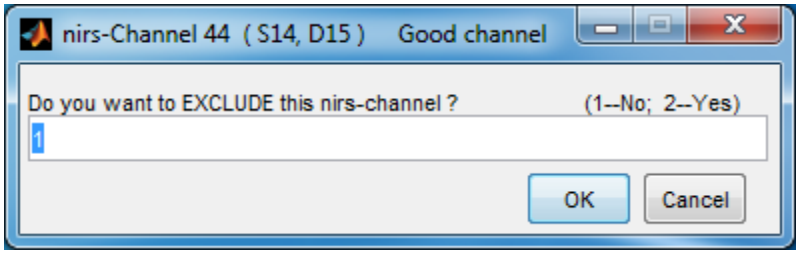


Figure 3-9. An example of the second pop-up that is generated, along with the raw-data plot shown in Figure 3-4, by clicking on the row of information highlighted in Figure 3-2.

If the channel that you select for inspection already is designated as 'bad', then the pop-up window will ask if you want to INCLUDE it, instead of whether you want to EXCLUDE it as in Figure 3-9. You are permitted to change the status of a channel any number of times; therefore, you need not be concerned about inadvertently excluding a good channel, or including a bad one, in any of the editing operations described in this user's manual section.

2 *Truncate Time series* GUI

Click on the *Truncate Time series* button to launch the GUI depicted in Figure 3-10. You can see that its appearance is – by design – very similar to that of the *Set markers* GUI described in Chap. 2. You may also notice that the number of event time intervals displayed in the plot window is smaller than in the

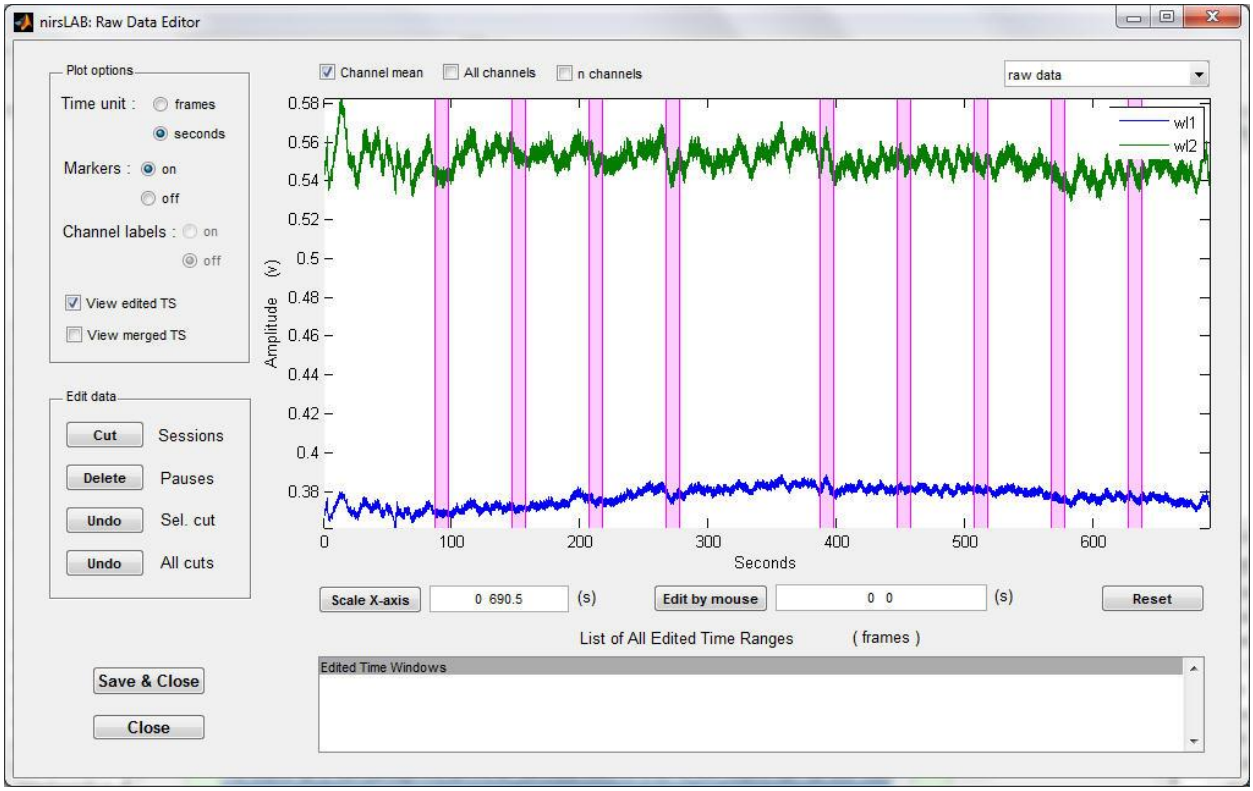


Figure 3-10. The *Truncate Time series* GUI, with its default display options selected. (Note that if, as here, the legend obstructs part of a plotted time series, you can simply click-and-drag it to a different part of the plot window.)

Chap. 2 figures relating to the same demo data set, and that the inter-event time interval is not constant. We have intentionally introduced these differences in order to facilitate the description, in Section 2.3, of functions available in the 'Edit data' module. Before getting to those, however, we will point out several important differences between the Figure 3-10 and *Set markers* GUIs.

2.1 Display options

- While the *Set markers* plot field shows all measurement channels having raw-data values larger than the threshold voltage (Chap. 2, Section 4.2), the *Truncate Time series* GUI (and in all others described in this and subsequent chapters) displays time series for only the channels that are defined in the probeInfo file (Chap. 7). Also, there is no minimum-value threshold. A different mechanism, described in the next item, is provided for controlling the number of time series plotted.

- In addition to the *Channel mean* and *All channels* checkboxes, this GUI offers a display option called *n channels*, as shown in Figure 3-11 (top). When this option is selected, the additional data fields shown in Figure 3-11 (middle) appear to the right of the *n channels* checkbox. The grayed-out field at the right displays the range of channels whose time series are shown in the plot window (the first 11, by default). The number in the enabled field at the left (10, by default) is the channel-range increment value: in the example considered here, the first time you click on the '▶' button of the scrollbar that lies between the number fields, the range of displayed channels will change from 1-19 to 11-30, as shown in Figure 3-11 (bottom).

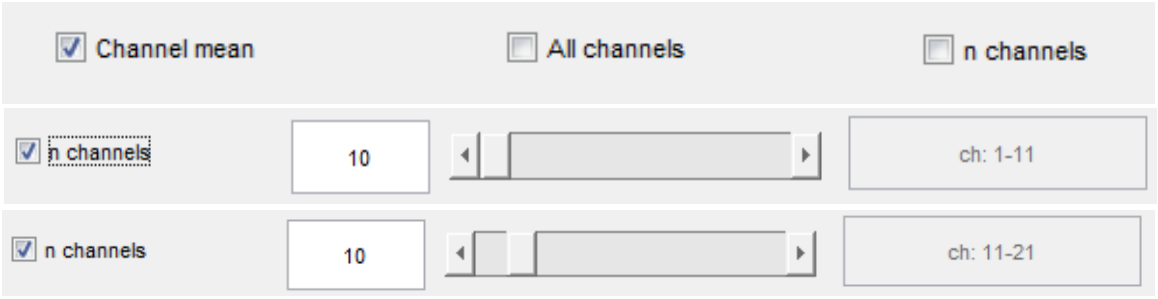


Figure 3-11. (Top) Display-options checkboxes in the *Truncate Time series* GUI. (Middle) Data fields that appear to the right of the *n channels* checkbox when that display option is selected. (Bottom) Clicking on the '▶' scrollbar button causes the range of channels displayed to increment by the number entered in the editable number field.

The smallest number that can be entered in the enabled number field is 1, from which it follows that there will always be at least two time series displayed in the plot window. The last channel in the current range becomes the first number in the range the next time you click on the '▶' button (*e.g.*, in Figure 3-11 the range changes from 1-19 to 11-30). Likewise, the last number in the range will become the first if you click on the '◀' button.

In addition to the '▶' and '◀' buttons, you can rapidly scroll through the set of channels in the probe setup by click-and-dragging the slide-bar to a desired position along the scrollbar.

- There are four options for scaling the plotted time-series data. These are accessed through a pull-down menu, shown enlarged in Figure 3-12, which you will find in the upper right corner of the *Truncate Time series* GUI. The menu items are:

  - raw data (default option): The units on the y-axis are the voltage values (proportional to intensities of light detected, as explained in the NIRStar 13.0 User Manual) that were are recorded in the project-specific '.wl1' and '.wl2' files.

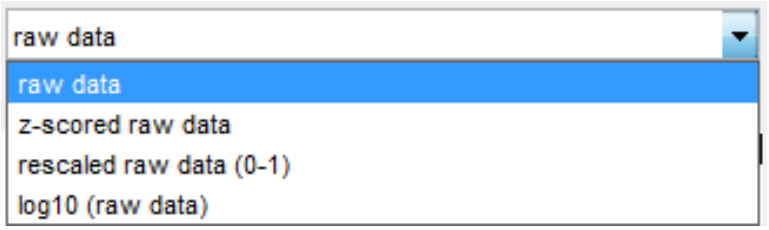


Figure 3-12. Pull-down menu for selecting among the data-scaling display options.

  - z-scored raw data: From the raw data (R) in each time series, nirsLAB computes the mean value (M_R) and standard deviation (S_R). The numerical values displayed on the y-axis are the z-scores [*i.e.*, $Z = (R - M_R)/S_R$] of the original data, and they are dimensionless. This plotting option can be helpful, for example, in cases where there is a large difference between the mean values or amplitudes of two time series, which makes it difficult to compare them. Note, however, that if you are displaying a large number of time series in the plot window, then the z-scored raw data might overlap to such an extent that it becomes difficult to visually resolve them.

  - rescaled raw data (0-1): From the raw data (R) in each time series, nirsLAB finds the minimum and (N_R) and maximum (X_R) values. The numerical values displayed on the y-axis are the raw data rescaled such that the minimum value is exactly 0 and the maximum values is exactly 1 [*i.e.*, $r_R = (R - N_R)/(X_R - N_R)$], and they are dimensionless. This plotting option can be helpful, for example, in cases where there is a large difference between the mean values or amplitudes of two time series.

  - log10(raw data): The numerical values displayed on the y-axis are the base-10 logarithms of the raw data. This plotting option can be helpful, for example, in cases where one time series in the plot window has raw-data values an order of magnitude larger than those for all the others; in the default display mode, all but one of the time series would be crowded together near the bottom of the plot window.

The four display options are illustrated in Figures 3-13, 3-14, 3-15 and 3-16, where, in order to avoid the problem of excessive overlap, we have chosen to display only two time series together. In addition, we plot only a fraction of the recorded measurement time, so that the high-frequency oscillations in the data will remain distinguishable when the two time series overlap.

2.2 'Plot options' module

The 'Plot options' module (default settings shown in Figure 3-13) allows you to select either frames or seconds as the display time unit, as described for the *Set parameters* GUI in Chap. 2, Section 4.1.

If the 'Markers: on' radio button is highlighted, then the event time intervals will be explicitly indicated by colored vertical bars in the plot window, as seen in Figures 3-2 and 3-5.

If the 'Channel labels: on' radio button is highlighted, then a legend will appear in the plot window, identifying the channels that correspond to the plotted curves, as shown in Figure 3-15.

The 'View edited TS' (**T**ime **S**eries) and 'View merged TS' options are not germane unless and until you delete time intervals from the data. Description of these options is therefore deferred to Section 2.3.

2.3 'Edit data' module

It is not an unusual occurrence, in a long fNIRS time-series measurement, that all of the data values you want to include in subsequent processing and analysis steps occur in only a portion of the overall recording time. Typical reasons why the data may include time intervals that you would want to truncate before proceeding include:

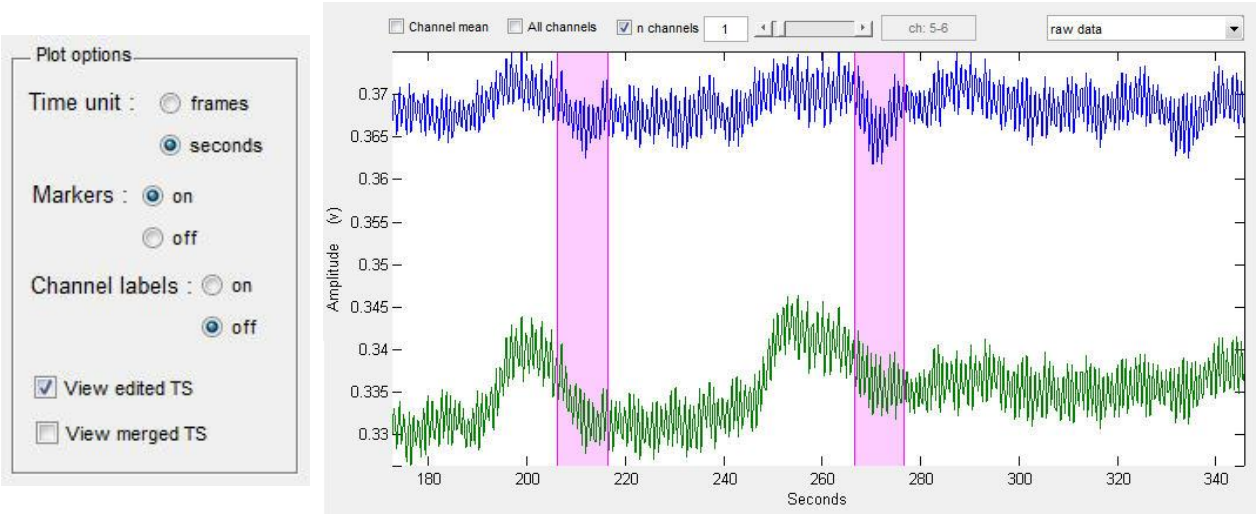


Figure 3-13. (Left) Default settings in the 'Plot options' module. Note that the 'Channel labels:' radio buttons are initially grayed out (see Figure 3-10), and become enabled only if you select the 'n channels' display option. (Below) An example of the *Truncate Time series* GUI's plot window, with default 'Plot options' settings and the default 'raw data' y-axis scaling option.

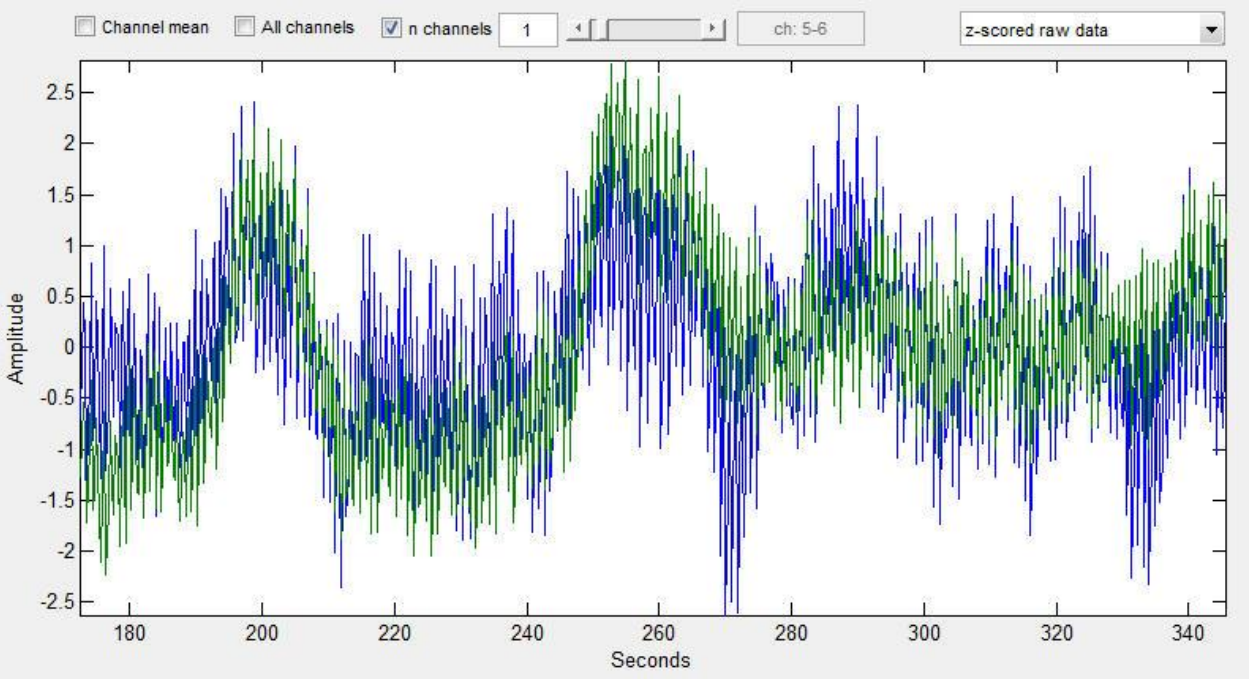


Figure 3-14. The *Truncate Time series* GUI's plot window, showing the same two time series as in Figure 3-13, but with 'Markers: off' selected in the 'Plot options' module and the 'z-scored raw data' y-axis scaling option.

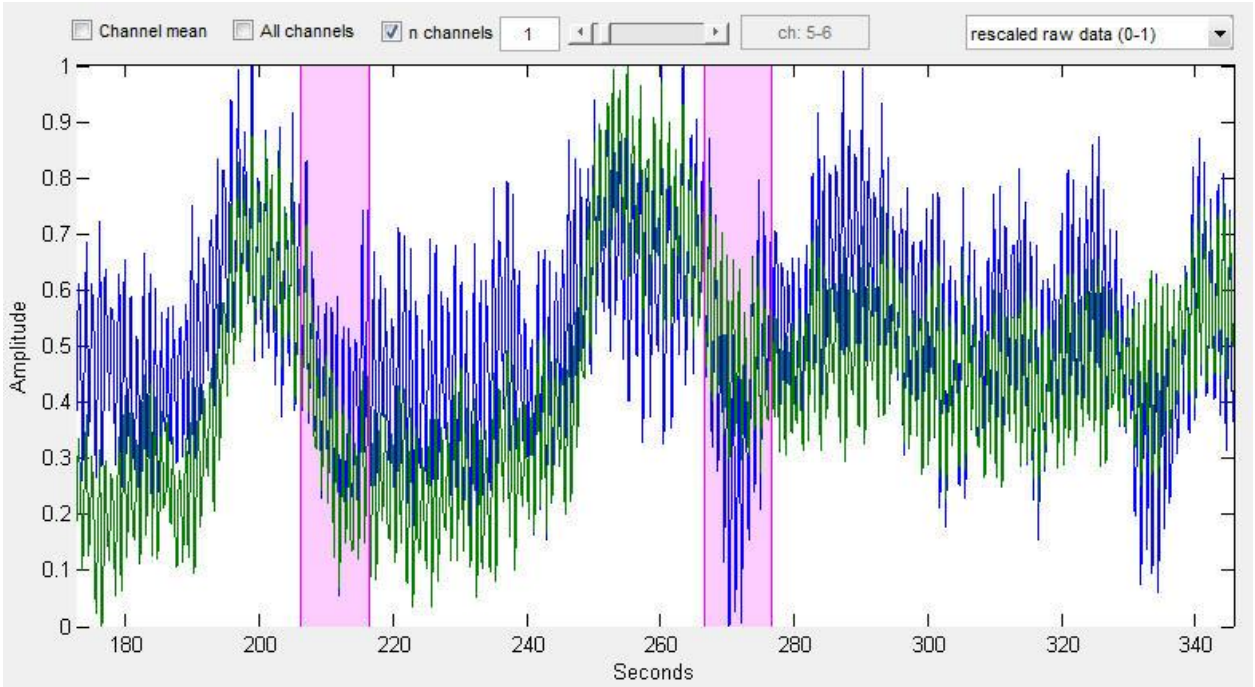


Figure 3-15. The *Truncate Time series* GUI's plot window, showing the same two time series as in Figure 3-13, but with 'Channel labels: on' selected in the 'Plot options' module and the 'rescaled raw data (0-1)' y-axis scaling option.

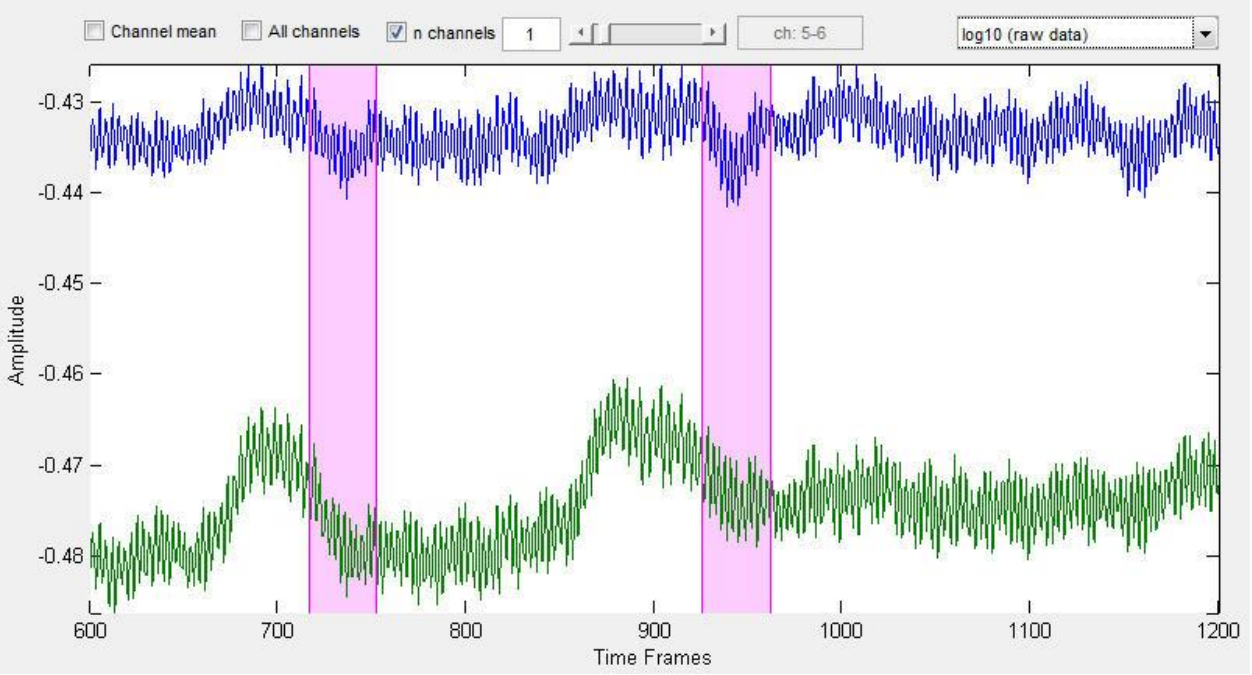


Figure 3-16. The *Truncate Time series* GUI's plot window, showing the same two time series as in Figure 3-13, with 'Time unit: frames', 'Markers: on' and 'Channel labels: on' selected in the 'Plot options' module and the 'log10(raw data)' y-axis scaling option.

- A resting baseline period of substantial duration preceded the first event episode, in order to ensure that the probe placement was stable and the subject was in a comfortable and relaxed state.
- A "cool-down" resting baseline was recorded after the end of the last event episode, to allow you to evaluate the magnitude of the long-term drift in the measurement channels.
- Multiple types of task or stimulus-presentation protocol were "bundled" into a single extended data-recording session (in some cases episodes of different event types occur in an alternating, or other intermixed, sequence), and you need to isolate the time intervals corresponding to a particular event-type of interest.
- There may have been extended interludes between episodes for a given event type: rest periods, practice sessions, times when the subject was receiving instructions, *etc*.

The functions that are accessed through the 'Edit data' module and the 'Edit by mouse' controls (all shown enlarged in Figure 3-17) allow you to remove time intervals that are not relevant to you. In cases where one or more interior time intervals are removed, the data on either side of the cut are merged together into a new, shorter time series. (This is where the 'View edited TS' and 'View merged TS' options alluded to in Section 2.2 become relevant.)

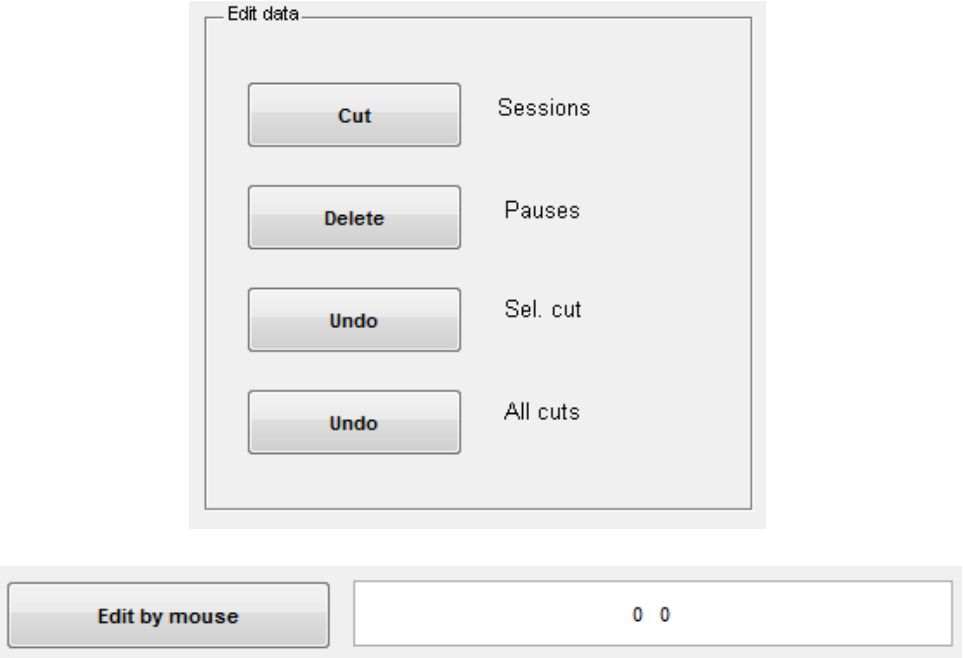


Figure 3-17. Detail views of the 'Edit data' module (top) and 'Edit by mouse' controls in the *Truncate Time series* GUI (Figure 3-10).

As pointed out in Chap. 1, Section 4.1, the nirsInfo file keeps track of all changes that you make, and this includes truncations of the data. Consequently, you will always be able to "undo" (see Figure 3-17), either in the current nirsLAB session, or in a subsequent one, any data truncations that you perform. Furthermore, the results of all operations performed by nirsLAB are stored in the nirsInfo file or in other, new files that are generated during the data-processing sequence. The original imager-generated files ('_config.txt', '.evt', '.set', '.wl1', '.wl2') are read but never modified.

- If there are time intervals that you want to remove from either end if the data time series (*e.g.*, initial or terminal baseline segments, as described above), click on the *Cut Sessions* button seen in Figure 3-17 to cause a pop-up window such as the ones shown in Figure 3-18 to open; notice that the time unit will match the one that you have selected in the 'Plot options' module. In addition, the default numerical values in the two fillable fields are equal to the amount of time that precedes the first Start marker (first row) and follows the last Stop marker (second row). (For the demo data set considered here, there are 299 measurement frames before the first Start marker and 188 following the last Stop marker. And at the 3.47 frames-per-second sampling rate, these correspond to approximately 86 and 55 seconds) That is, the default setting is that no data points should be truncated from either end of the time series.

For concreteness, suppose that you choose to truncate the first 199 and last 88 time frames, to produce time series with equal-length initial and terminal baseline segments of 100 frames (~30 s) duration. When you type '100' into both fields of the pop-up window and click the *OK* button, the plot-window

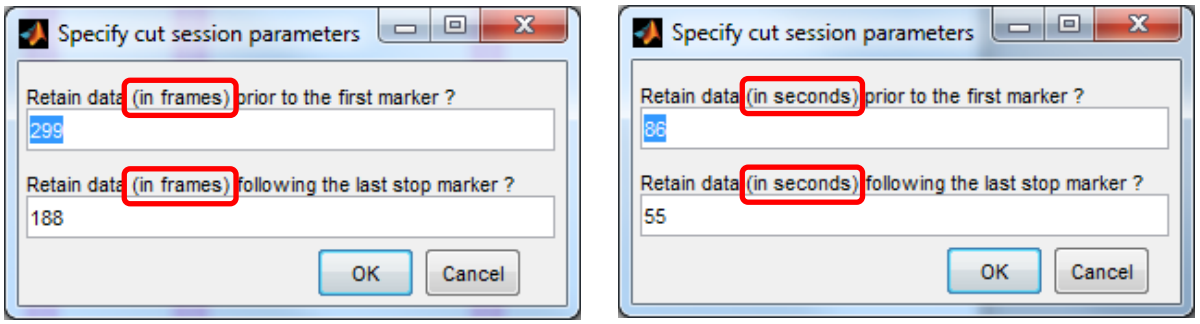

Specify cut session parameters
Retain data (in frames) prior to the first marker ?
299
Retain data (in frames) following the last stop marker ?
188
OK
Cancel
Specify cut session parameters
Retain data (in seconds) prior to the first marker ?
88
Retain data (in seconds) following the last stop marker ?
55
OK
Cancel

Figure 3-18. Examples of the pop-up window that opens when the *Cut Sessions* button (see Figure 3-17) is clicked. The time unit is the same as the one that the user has selected in the 'Plot options' module.

display changes in the manner shown in Figure 3-19 (where the 'Channel mean', 'Markers: off', and 'z-scored raw data' plot options have been selected). When you click on a row in the 'List of All Edited time Ranges' field (Figure 3-20), the corresponding time interval is highlighted in the plot window, as shown in

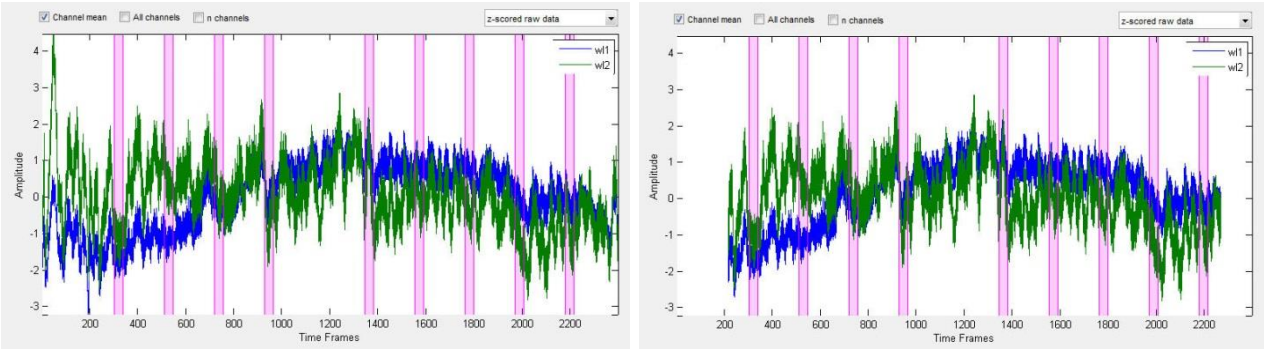


Figure 3-19. Time series displayed in the plot window before (left) and after (right) truncation of the first 199 and last 88 time frames.

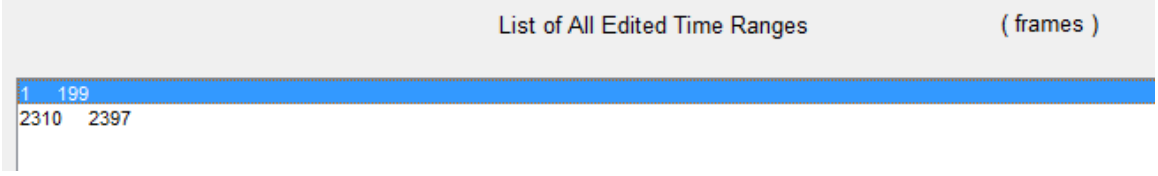


Figure 3-20. Detail from the 'List of All Edited Time Ranges' field, after the first 199 and last 88 time frames have been truncated.

Figure 3-21. If it turns out that the highlighted time interval is not actually the one that you wanted to truncate, you can cancel it by clicking on the *Undo Sel. Cut* button in the 'Edit data' module (Figure 3-17).

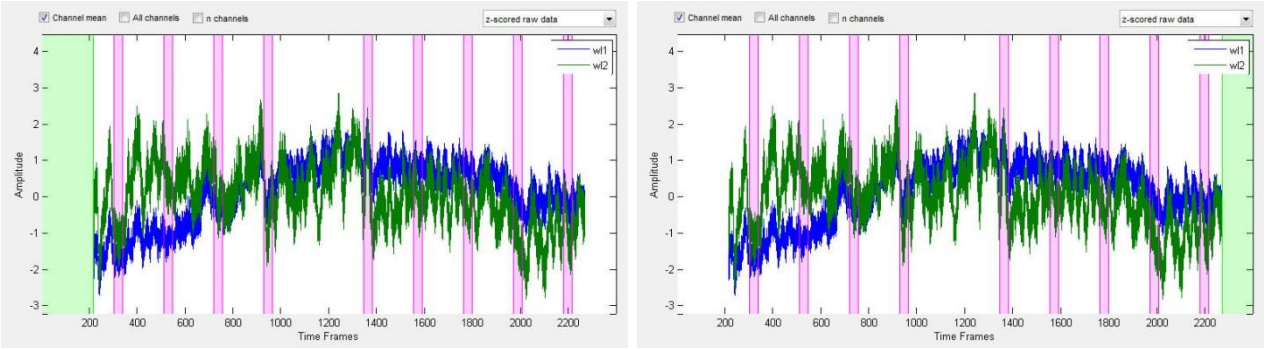


Figure 3-21. Selecting a row in the 'List of All Edited Time Ranges' field (Figure 3-20) highlights the corresponding time interval in the plot window.

To see what the edited time series will look like after the truncation process is finalized, click in the 'View merged TS' checkbox in the 'Plot options' module (Figure 3-13). The result for this example is shown in Figure 3-22, which also indicates how the duration of the time series is automatically adjusted.

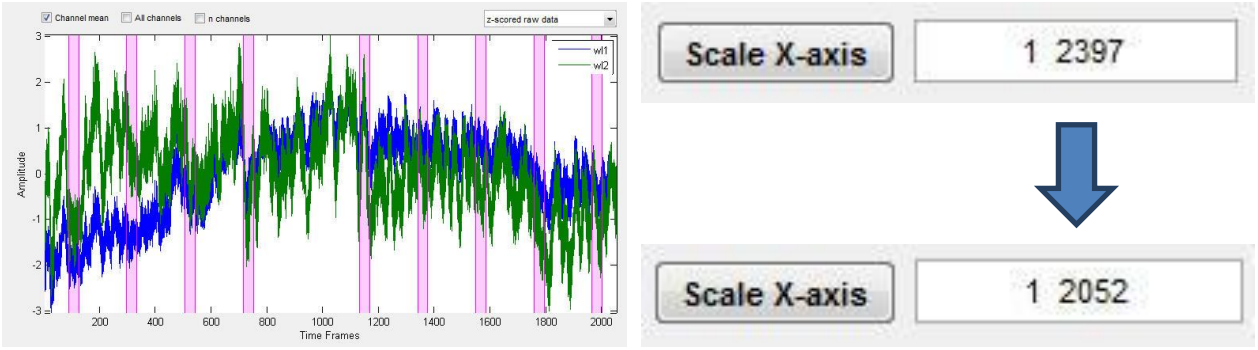


Figure 3-22. (Left) Clicking the 'View merged TS' checkbox (Figure 3-13) updates the view in the plot window, to show the edited time series with the selected time intervals truncated. (Right) The default x-axis limits are automatically updated to reflect the fact that there are fewer time frames in the truncated time series (top/ bottom = before/after truncation).

- *Delete Pauses* is a useful editing tool for data sets in which the time intervals between successive event episodes is not uniform for the event-type you want to analyze. As suggested earlier in this Section, reasons why this can occur include (but are not limited to) protocols wherein episodes of multiple event types occur in an intermixed sequence, or when there are one or more rest periods during the measurement session. The tool will produce a modified set of time series with a constant inter-event time interval.

Click on the *Delete Pauses* button in the 'Edit data' module (Figure 3-17) to open a pop-up window such as the one shown in Figure 3-23. Note that that the time unit here is always seconds. We therefore recommend that you select seconds as the time unit in the 'Plot options' module, so that you can use the numbers on the x-axis of the plot window to guide your selection of values to type into the number fields.

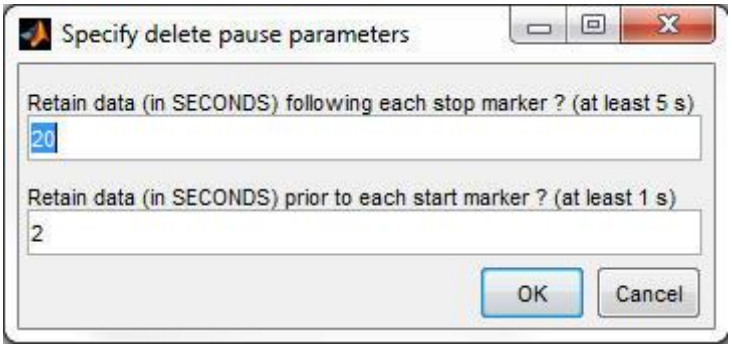

Specify delete pause parameters
Retain data (in SECONDS) following each stop marker ? (at least 5 s)
20
Retain data (in SECONDS) prior to each start marker ? (at least 1 s)
2
OK
Cancel

Figure 3-23. Example of the pop-up window that opens when the *Delete Pauses* button (see Figure 3-17) is clicked.

In the example plot window shown in Figure 3-24, you will notice that most of the inter-event time intervals are of about 50-seconds duration. The fourth interval is an exception, and lasts for approximately 110 s. To demonstrate the use of the *Pause Sessions* tool, let's say that we want to impose a uniform 30-s duration on the inter-event intervals [*e.g.*, in order to facilitate subsequent block averaging (Chap. 5) or generation of GLM design matrices (Chap. 6)]. One way

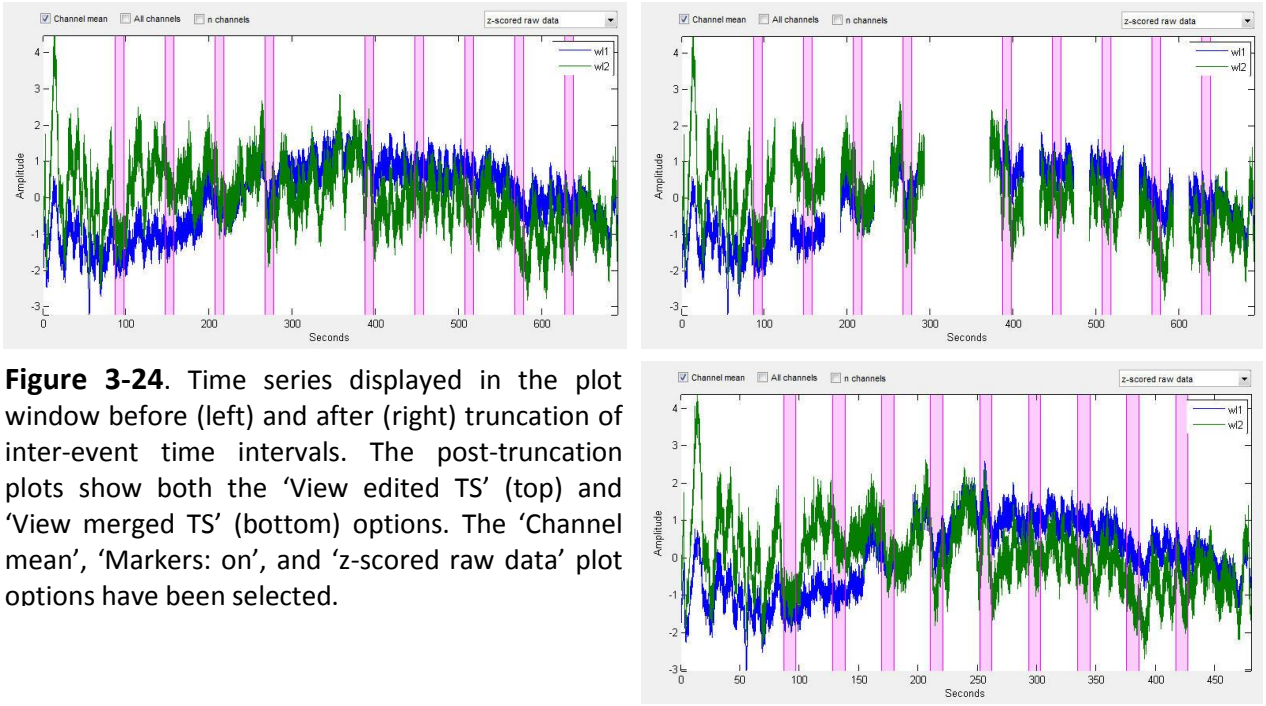


Figure 3-24. Time series displayed in the plot window before (left) and after (right) truncation of inter-event time intervals. The post-truncation plots show both the 'View edited TS' (top) and 'View merged TS' (bottom) options. The 'Channel mean', 'Markers: on', and 'z-scored raw data' plot options have been selected.

to accomplish this is to enter '15' in both number fields of the pop-up window. When we click on the *OK* button, the plot updates to show blank spaces in all of the time intervals that are marked for removal. Click in the 'View merged TS' checkbox in the 'Plot options' module (Figure 3-13) to preview the edited time series that will result when the data in the remaining time intervals are joined end-to-end.

In the preceding example we chose to delete time intervals that were centrally located between pairs of adjacent events. However, this is not a requirement of nirsLAB. We also could have obtained a uniform 30-s duration for the inter-event intervals by entering '20' and '10' in the upper and lower number fields, respectively, or '10' and '20', '5' and '25', or any other combination that sums to 30. The only restrictions are that, as you can see in Figure 3-23, you must keep at least 5 seconds of data immediately following each Stop marker and at least 1 second of data immediately preceding each Start marker.

The starting and ending times, in seconds, for all time intervals marked for deletion are shown in the 'List of All Edited time Ranges' field (Figure 3-25). Clicking on any row will highlight the corresponding interval in the plot window, just as in the previously discussed *Cut Sessions* case (see Figure 3-21). If a highlighted time interval is one that you do not wish to delete after all, click on the *Undo Sel. Cut* button in the 'Edit data' module (Figure 3-17) to remove it from the

Figure 3-25. Detail from the 'List of All Edited Time Ranges' field, after all inter-event time intervals have been truncated to 30-seconds duration, indicating the ranges of time that have been deleted.

Please also note that, if the nirsInfo file for your project contains temporal marker information for two or more event types, then the *Delete Pauses* tool will edit the time intervals between all adjacent pairs of event time intervals, whether they correspond to the same event type or to different ones! If this is not what you want, convenient ways to avoid it are:

- Use the *Undo Sel. Cut* button, as described in the preceding paragraph, to remove the unintended deletions.
- Prepare multiple copies of the imager-generated files, in separate folders. Generate a nirsInfo file in each one. (If the '.wl1' and '.wl2' files consume significant amounts of hard-disk space, you

may delete them after the nirsInfo files have been generated, while always retaining one master copy for your records.) For each nirsInfo file, delete all but one type of event using the *Delete Condition* tool described in Chap. 2, Section 4.3.

- Use the *Edit by mouse* tool, described next, instead of *Delete Pauses*.
- The function of the *Edit by mouse* tool is similar to that of *Delete Pauses*, in that it allows you to specify interior time intervals to delete from your data. However, instead of acting on all inter-event time intervals, it acts on particular intervals that you specify, one at a time.

  The instructions for using the *Edit by mouse* tool are – by design – very similar to those for zooming in and out on the x-axis display range, as described in Chap. 2, Section 4.2. You may either directly type the starting and ending times for the interval that you want to delete into the *Edit by mouse* number field (Figure 3-17), or click on the *Edit by mouse* button (Figure 3-17) to activate plot-window crosshairs, which you will then use to select the starting and ending times by clicking on them. An example, illustrating the use of this approach to delete a portion of the extra-long inter-event time interval, is shown in Figure 3-26.

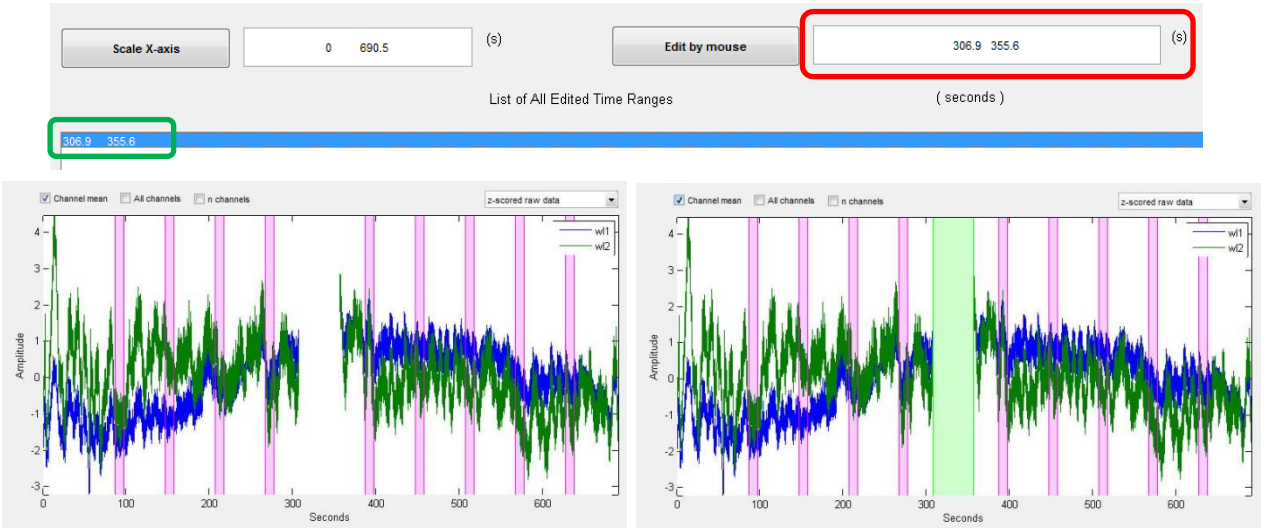


Figure 3-26. (Top) The starting and ending times for a truncation time interval were typed directly into the *Edit by Mouse* number field (within red oval), and also are indicated in the 'List of All edited Time Ranges' field (within green oval). (Bottom) nirsLAB automatically blanks out data in the selected time interval when the user specifies its starting and ending times (left), and clicking on any row in the 'List of All edited Time Ranges' field highlights that time interval in the plot window (right).

2.4 Additional Considerations

- Impact of Long-term Trends in Data Time Series. In the demo data set considered here, the time series do not exhibit any significant slow drifts from the beginning to the end of the measurement. However, you should not be surprised if in some cases, your fNIRS data do contain long-term trends. (Indeed, the possibility of such is one of the reasons why, as discussed

at the start of Section 2.3, experimental protocols frequently feature initial and terminal baseline time intervals.) If drifts are present in the data that you are editing, one impact that they potentially could have is to introduce discontinuities ("jumps", "steps") into the edited time series when the data on either side of a truncated interior time interval are merged. To prevent this from happening, nirsLAB automatically adds or subtracts a constant from the raw data values that precede a truncated segment, in order to equalize the raw data values on either side of that segment. This process is illustrated in Figure 3-27.

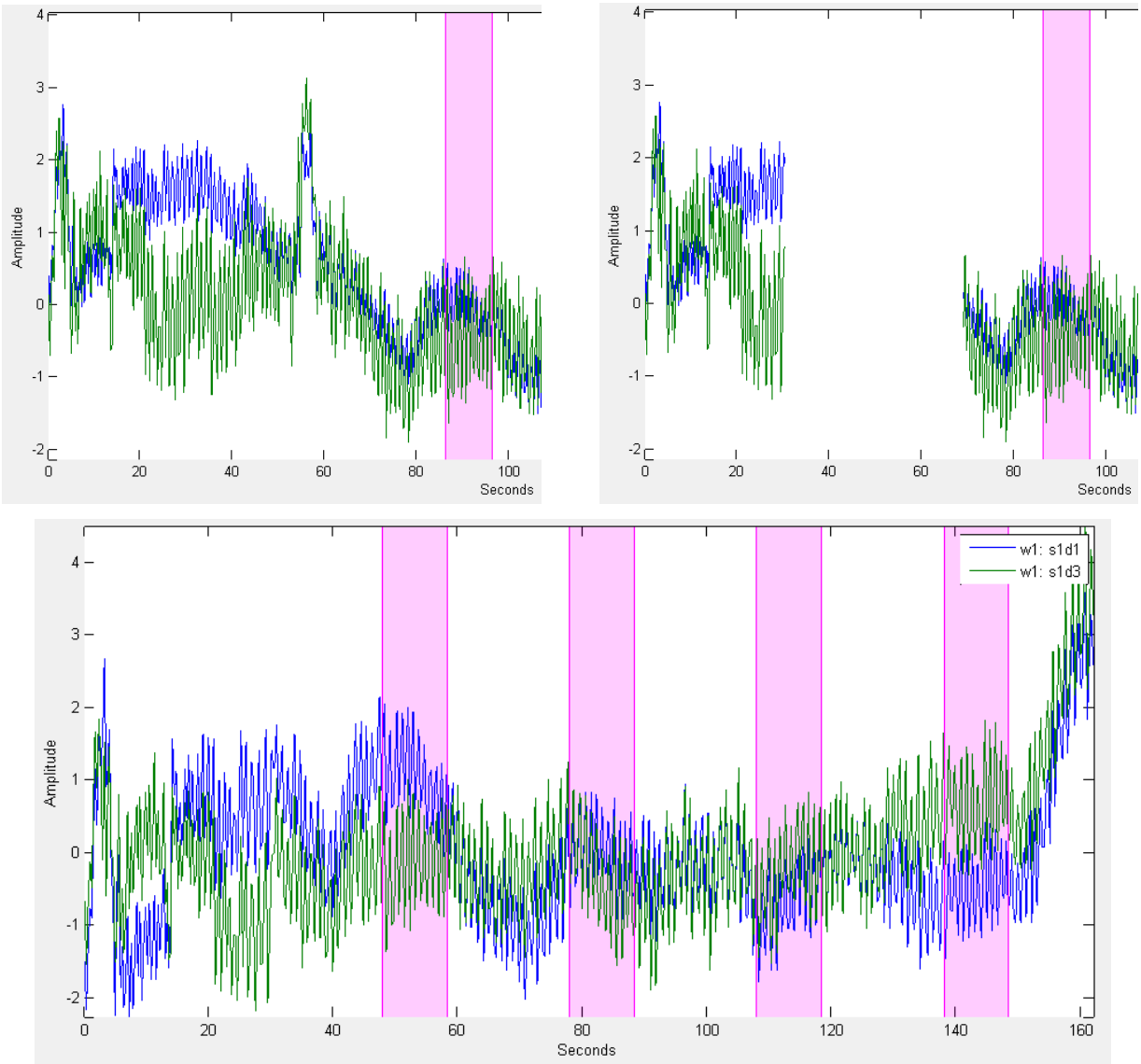


Figure 3-27. (Top left) Original data, prior to truncation. (Top right) If the data on either side of the truncated segment were merged "as is", there would be step discontinuities in the resulting edited time series. (Bottom) nirsLAB automatically subtracts a constant amount from the portion of the data that precedes the truncated segment, so there are discontinuities in the merged time series.

- *Undo All cuts* button. Pressing the *Undo All cuts* button (see Figure 3-17) in the 'Edit data' module will cancel all editing operations performed in the current nirsLAB session, or in previous ones. (The *Undo Sel. Cut* function also can be applied to truncations carried out during previous sessions.)
- *Save & Close*, *Close* buttons. To implement the truncation operations you have specified in *Truncate Time series*, click on the *Save & Close* button near the lower-left corner of the GUI (see Figure 3-10). To exit from the GUI without implementing the truncations, click on the *Close* button instead.

3 *Remove Discontinuities* GUI

Click on the *Remove Discontinuities* button in the *Data Preprocessing* portal (Figure 3-1) to launch the GUI depicted in Figure 3-28. You can see that its appearance is very similar to that of the *Truncate time series* GUI described in Section 2; the GUI controls and options lying within green dashed-line ovals in

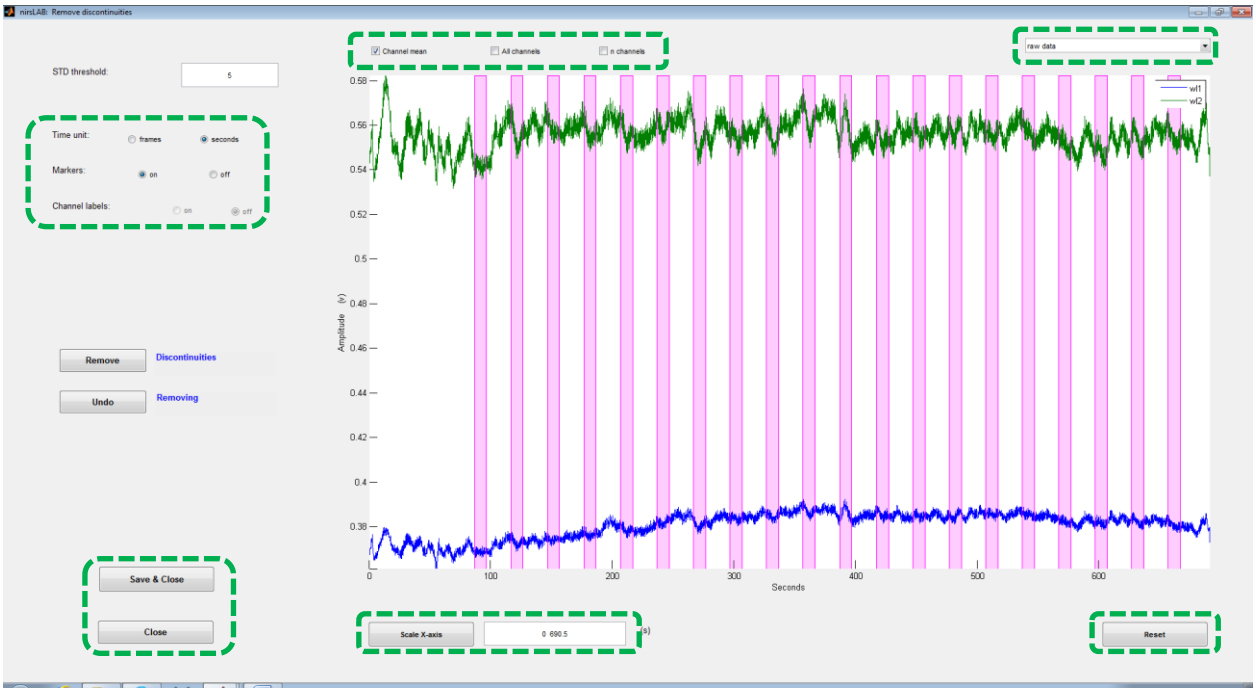


Figure 3-28. The *Remove Discontinuities* GUI, with its default display options selected.

Figure 3-28 are identical to the corresponding features seen in Figure 3-10. While the channel-mean time series displayed in the plot window are not noticeably different from those used for demonstration purposes up to this point, the data set that we are using to illustrate the *Remove Discontinuities* functionality ('demo2' sub-folder *filename* = 'demojumps') contains discontinuities, which we have intentionally introduced, in 8 out of the 44 channels defined during probe setup (Chap. 7). Two of these

artifacts are identified in Figure 3-29 (blue ovals), where we also highlight the features that are unique to *Remove Discontinuities* (red dashed-line ovals). It is important to correct for artifacts of this type in time-series data (and likewise for the "spike" artifacts that are addressed in Section 4, because it has been

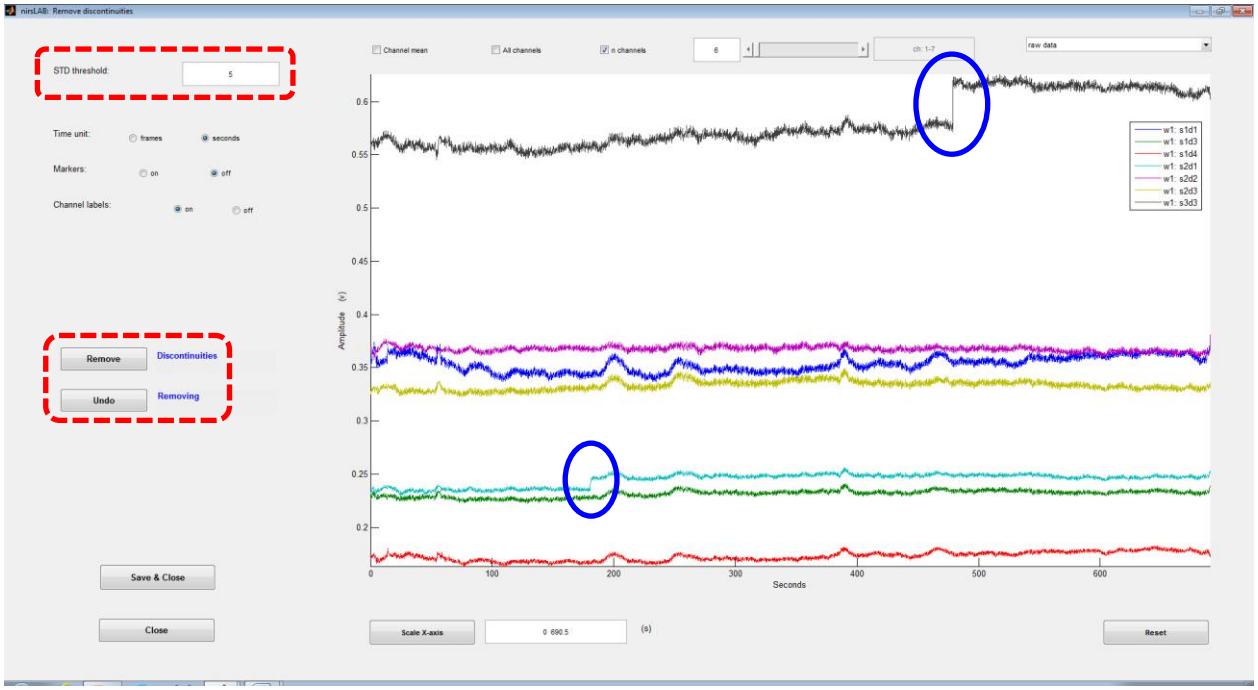


Figure 3-29. Identification of the unique features of the *Remove Discontinuities* GUI. A number of artifacts are evident in the individual-channel time series.

shown that in the absence of any correction, significant artifacts can remain in block averages (*i.e.*, temporal mean) over many event episodes, even if only a fraction of the individual blocks are contaminated, and that these residual artifacts can induce significant biases in results obtained from subsequent statistical analyses such as GLM computations.[1] Fortunately, our experience has been that users of NIRx imaging equipment can obtain high-quality measurements data, where the number of serious artifacts is small enough that the implicated channels and/or time intervals can simply be excluded from further consideration without compromising their ability to perform the intended analyses. However, for cases where this preferred remedy would be unsatisfactory, nirsLAB provides tools for ameliorating the most commonly seen types of data artifacts.

The method that nirsLAB implements to reduce artifacts of this type seen in Figure 3-29 is:

1. From the raw data (R) in each time series, the standard deviation (S_R) is computed.
2. For each pair of successive data values (R_i and R_{i+1}), the ratio of the difference to the standard deviation $[(R_{i+1} - R_i)/S_R]$is calculated. We will call this ratio J_i.
3. All locations in the time series where J_i is at least as large as the user-specified value in the 'STD threshold:' field (shown enlarged in Figure 3-30) are identified. Note that the value you type in

this field does not have to be a whole number (*e.g.*, values of 1.1, 1.9, 2.5, *etc*., are acceptable), but it cannot be smaller than 1.

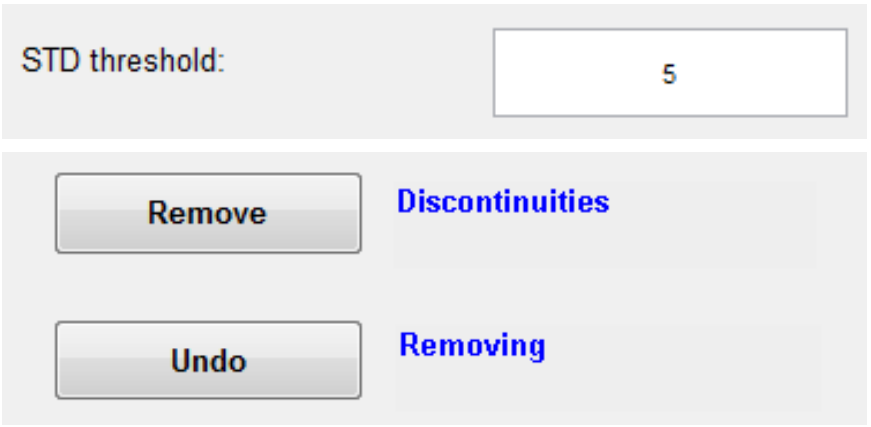


Figure 3-30. Detail view of the function-specific features in the *Remove Discontinuities* GUI. We use STD threshold values of (default value; see Figure 3-29) and 4 to produce the results shown in Figures 3-31 and 3-32, respectively.

4. Starting with R_{i+1}, a constant value is subtracted from all data values following the jump: $R'_k = R_k - (R_{i+1} - R_i)$. This action takes place when you click on the *Remove Discontinuities* button shown in Figure 3-30, and the plot-window display automatically updates to show both the original time series (in gray) and the edited one (in the original color).

In Figure 3-31 we show the effect of the preceding algorithm on the time series considered here, when the STD threshold is set to 5 as shown in Figure 3-30. It is seen that the larger of the discontinuities highlighted in Figure 3-29 has been eliminated (black curve), but the smaller one (light blue curve) has not. However, by lowering the STD threshold to 4, the second discontinuity also is removed, as shown in Figure 3-32.

While the algorithm described here has produced satisfactory results when applied to the demo dataset, there are performance tradeoffs that you may encounter in practice and should should keep in mind:

- Since the artifact-identification process (Step 3 above) is based on individual values of J_i, the algorithm does not distinguish between large-amplitude "jumps" and large-amplitude "spikes," and the same action (Step 4) will be performed in both cases. In the spike case, the net effect of this could be to actually introduce a jump where there wasn't one originally. If you are preprocessing a data set that contains both types of artifact, we recommend that you reduce the spikes first, using the tools in either *Truncate Time series* (Section 2) or *Remove Spike artifacts* (Section 4) before applying *Remove Discontinuities*.
- Sometimes a "jump" has the appearance of an abrupt change in value when you view the entire time series, but in reality it develops over several time frames, and if you zoom in on the time axis you will see that the detector-reading value changes more gradually than it had appeared to in your initial inspection. In a case like this, it may turn out that there is no single time-frame

"jump" that exceeds the STD threshold, and you may need to lower it for the algorithm to have any effect on the artifact. But if the threshold is lowered too much, then data features that are not artifacts may be incorrectly identified as artifacts. Remember to always inspect the time series for all channels after performing a discontinuity correction, to ensure that it has not introduced spurious features into your data.

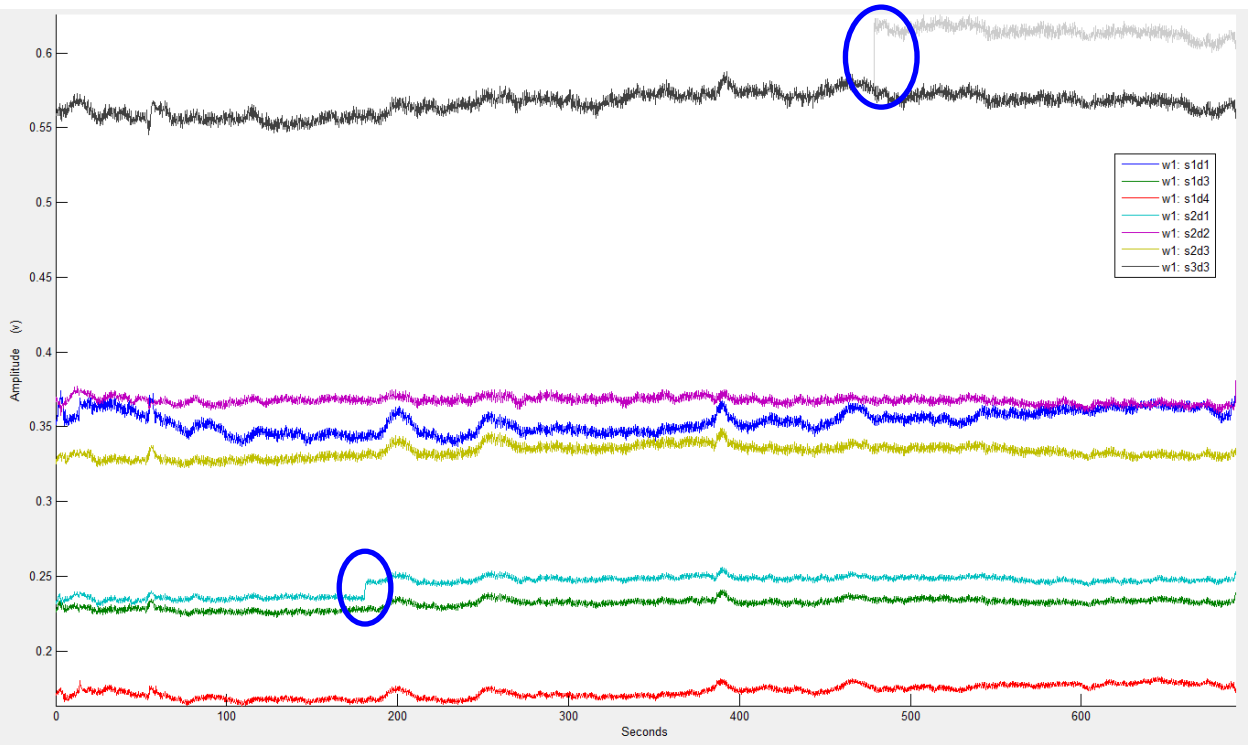


Figure 3-31. Result obtained after clicking *Remove Discontinuities* (Figure 3-30) when the STD threshold value is set at 5. Gray curve = original (pre-correction) time series.

- The demo data used for this illustration exhibits very little long-term trend. But in some cases you may find that there are substantial levels of drift in some of the data channels. If this occurs, it will have the effect of increasing the value of S_R (Step 1 above), and this will impair the algorithm's ability to identify discontinuities. We expect that subsequent releases of nirsLAB will include more sophisticated algorithms, currently in development,[2] for identifying and correcting discontinuities, as well as artifacts of the type considered in Section 4.

If you are not satisfied with the outcome of a discontinuity correction, you can restore the original data (at any time during the current or future nirsLAB sessions) simply by clicking on the *Undo Removing* button shown enlarged in Figure 3-30. If you want to change the value of the STD threshold, it is not necessary to explicitly undo the previous result first; simply type the new value into the 'STF threshold:' field and click on the *Remove Discontinuities* button.

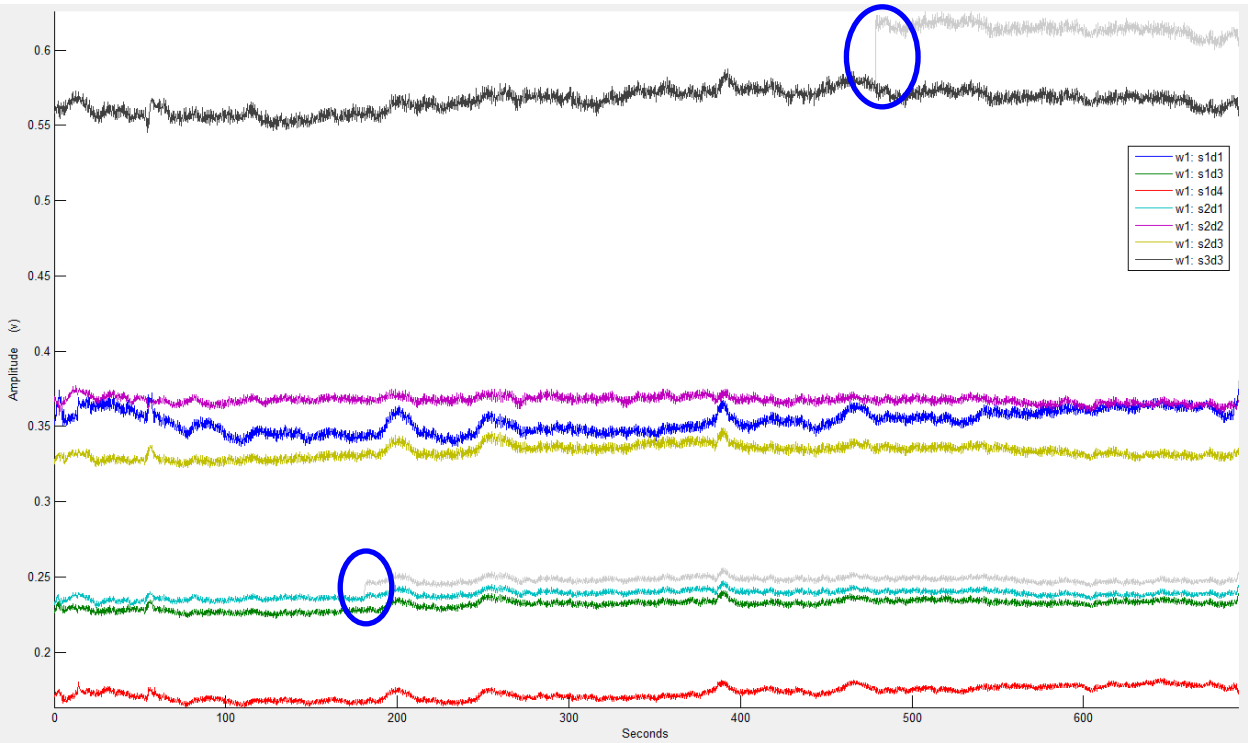


Figure 3-32. Result obtained after clicking *Remove Discontinuities* (Figure 3-30) when the STD threshold value is set at 4. Gray curves = original (pre-correction) time series.

4 *Remove Spike artifacts* GUI

Click on the *Remove Spike artifacts* button in the *Data Preprocessing* portal (Figure 3-1) to launch the GUI depicted in Figure 3-33. The features that are unique to this GUI are contained within the red dashed-line oval, and the controls used to select artifact-contaminated time intervals are located within the blue dashed-line oval. The data files used for demonstration purposes here are found in the 'demo2' sub-folder (*filename* = 'demospikes'). The specific data time series that we focus on to illustrate the impact of the effects of the *Remove Spike artifacts* process are shown in Figure 3-34. You can see that two of the three displayed time series contain several isolated spikes and a number of spike clusters. The spike-reduction strategies implemented in the current nirsLAB release are similar to the method described in Section 2.3. The key difference is that *Remove Spike artifacts* does not produce edited time series having decreased length. Instead, it fills in the specified time interval with imputed data values,[3] so that there is no change in the number of measurement frames. This can be an important consideration if, for example, an artifact-contaminated interval occurs during an event episode and truncating it would complicate the computation of block averages. An additional practical benefit to leaving the time-series length unchanged is that you will thereby avoid the possibility, discussed in Section 2.4, of new discontinuities appearing as a consequence of long-term drifts in the data.

To start the process of removing spikes, specify a time interval of interest by using either of the same two methods described in Section 2.3 for truncating a single interior time interval. That is, you can either type starting and ending times directly into the number field highlighted in Figure 3-33 (which is shown

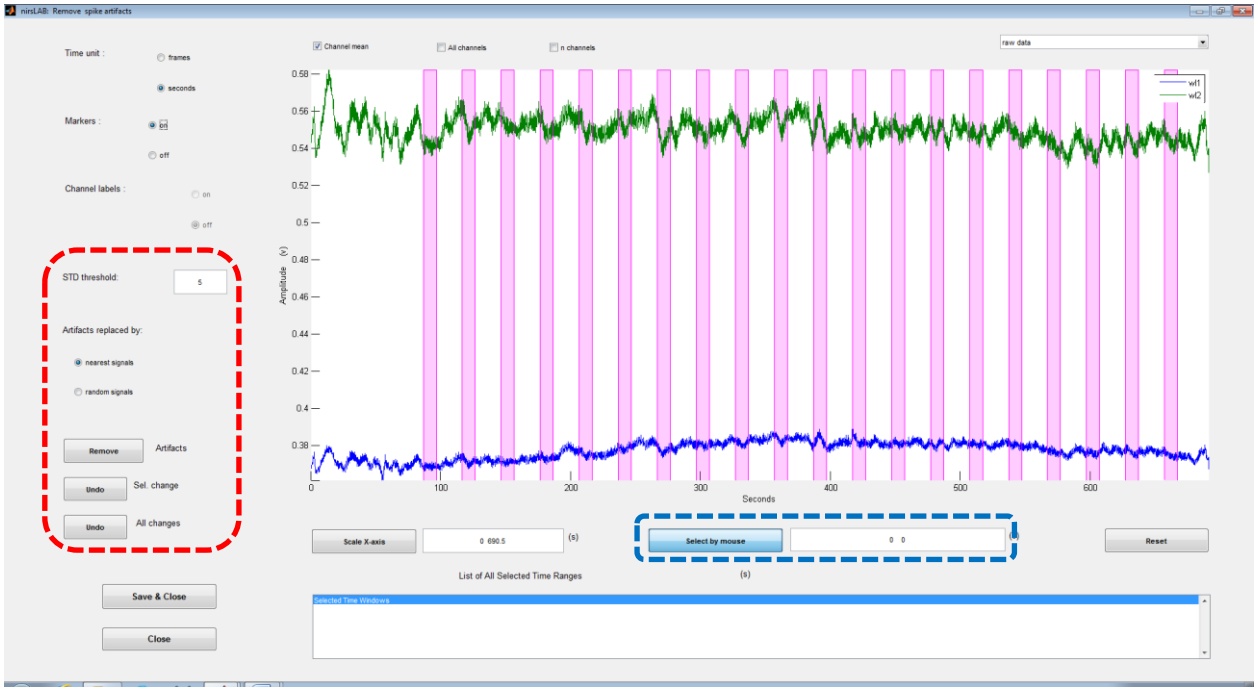


Figure 3-33. The *Remove Spike artifacts* GUI, with its default display options selected.

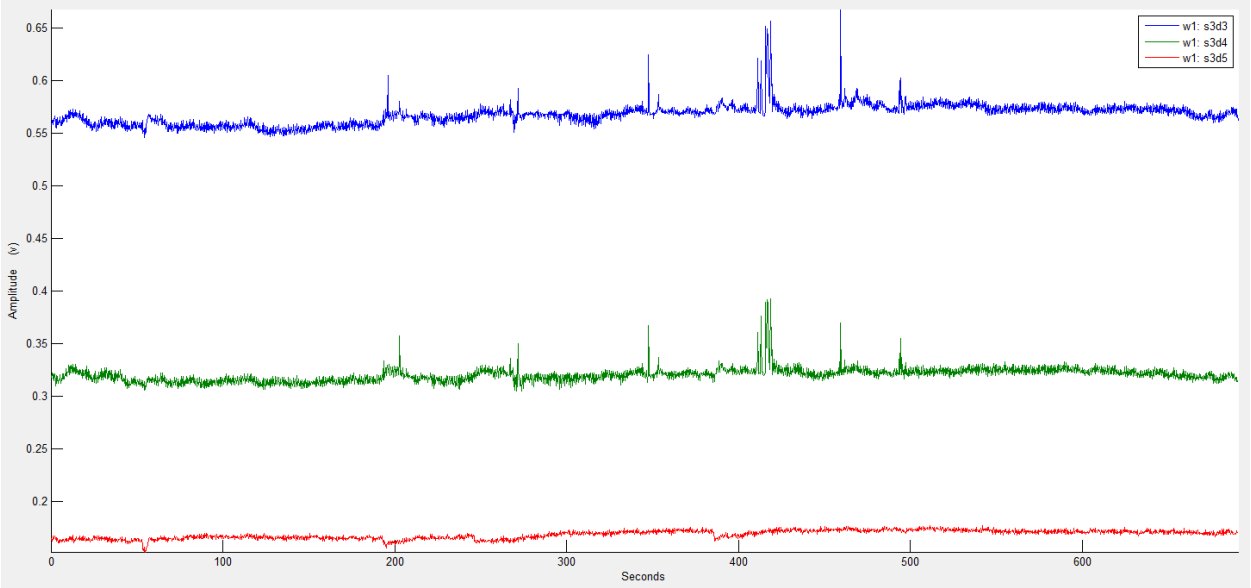


Figure 3-34. Three specific time series selected to illustrate performance of the *Remove Spike artifacts* GUI. Two contain multiple large-amplitude artifacts, while the third is comparatively artifact-free.

enlarged in Figure 3-35), or else click on the *Select by mouse* button to activate crosshairs that you then use to select the starting and ending times.

You can see in Figure 3-35 that nirsLAB offers two options for the data-imputation algorithm. The default option is 'Artifacts replaced by: nearest signals', and it is linked to the numerical value in the 'STD

Figure 3-35. Detail view of the portions of the *Remove Spike artifacts* GUI (Figure 3-33) that are used to specify and process spike-contaminated time intervals.

threshold:' field (default value = 5). If you use this method, then, after you select the artifact-spanning time interval(s) and click on the *Remove Artifacts* button shown in Figure 3-35 (according to your preference, you can either do this after each individual interval-selection step, or specify multiple intervals and then correct all them of them at once), nirsLAB will:

1. For every data channel and every selected time interval, find the maximum raw-data value *X* and minimum value *N*, and compute the difference: $D = X - N$.
2. Compute the standard deviation *S* of the raw data values, over the entire time series, for each channel. (If artifacts occupy only a small percentage of the measurement time frames, then their presence should not noticeably affect the value of *S*.)
3. Compute, for each selected time interval and channel, the ratio *D*/*S*. we will call this ratio *K*. If *K* is ≥ the specified STD threshold value, then an artifact is present. For every combination of time interval and channel that contains an artifact, nirsLAB carries out the following steps:

4. Identifies the two channels that are the nearest neighbors of the artifact-corrupted channel. If one or both of these also has an artifact in the same time interval, it is dropped from consideration and the next nearest neighbor is used instead. (This process is iterated until nirsLAB identifies two channels that are "clean" in the relevant time interval.)
5. Averages the raw-data values for the two neighboring channels, within the time interval under consideration.
6. Replaces the artifact-corrupted data with the average computed in Step 5. As needed, a constant value is added to the Step-5 result so that its mean value will equal the average of the original raw-data values that immediately precede and immediately follow the considered time interval.

The second data-imputation option is 'Artifacts replaced by: nearest signals'. If you select this method then, when you click on the *Remove Artifacts* button shown in Figure 3-35 (according to your preference, you can either do this after each individual interval-selection step, or specify multiple intervals and then correct all them of them at once), nirsLAB will:

1. Compute the standard deviation of the data values in the 4-second time intervals preceding and following the time interval you have specified.
2. Compute, as imputed data for the selected time interval, a set of random numbers that are sampled from a Gaussian distribution, with a standard deviation equal to the average of the two 4-second standard deviations computed in Step 1, and with a mean equal to R_p, where R_p stands for the data value that immediately precedes the time interval you have selected.
3. Substitute the imputed values computed in Step 2 for the original data values in the time interval you have selected.
4. Subtract a constant offset from all data values that follow the time interval you have selected, so that the spike-removal process will not have the effect of possibly introducing a new discontinuity. The value of the offset is $(R_f - R_p)$, where R_f stands for the data value that immediately follows the time interval you have selected.
5. To prevent the possibility of the imputed data values biasing results obtained in subsequent statistical analyses, the preceding steps are applied to all of the channels' time series in the data set, at both wavelengths, not only to the one that you focused on when specifying the artifact-contaminated time interval. An additional practical benefit to this is that, when artifacts of this type are present at all, in many cases they occur simultaneously in multiple data channels. Applying the correction procedure to all channels spares you from having to spend the time to process them one at a time.

In Figure 3-36 we show the results of applying *Remove Spike artifacts* to the trio of time series that are shown in Figure 3-34, using both data-imputation methods. As with other GUIs described in this chapter, any of the affected time intervals can be highlighted by clicking on the corresponding row in the 'List of All Selected Time Ranges' field. In addition, if you are not satisfied with the results of any artifact

corrections, you can cancel any of them by first highlighting it, as illustrated in the lower panel of Figure 3-36, and then clicking on the *Undo Sel. Change* button seen in Figure 3-35. You also can cancel all of them at a single stroke, by clicking on the *Undo All changes* button seen in Figure 3-35.

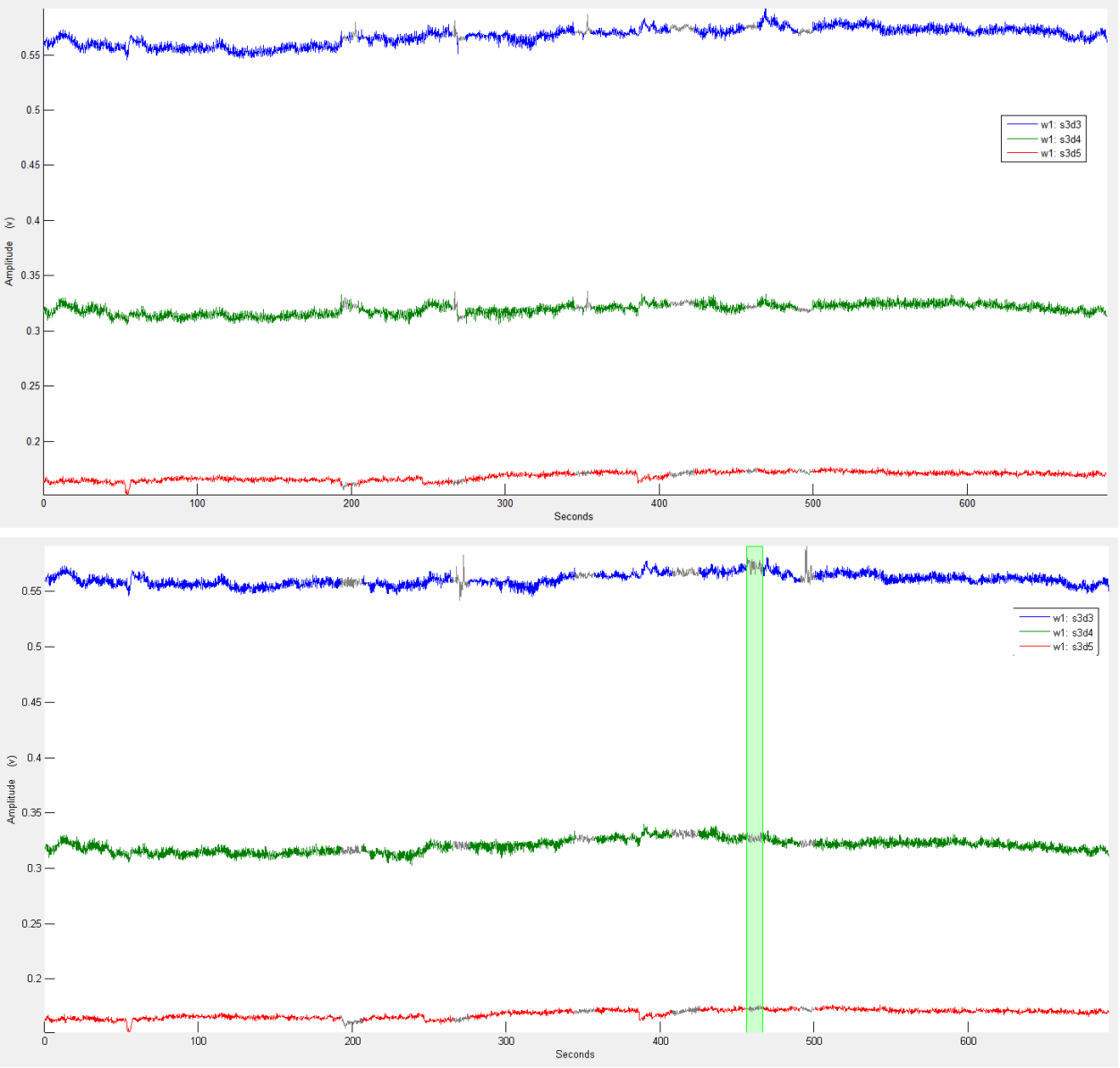


Figure 3-36. The same three time series as shown in Figure 3-34, after application of the *Remove Spike artifacts* procedure. Both the 'nearest signals' (top) and 'random signals' (bottom) data-imputation methods are used. In all cases, the imputed data values are shown in gray instead of in the original

Other approaches to spike-removal that are more sophisticated than the one presented here can certainly be envisioned, and implementations of some alternatives are either already available**Error!**

ookmark not defined. or are in development[2]. We expect that you will be able to select from among more than one alternative in future releases of nirsLAB.

5 *Apply Frequency filter* GUI

Click on the *Apply Frequency filter* button in the *Data Preprocessing* portal (Figure 3-1) to launch the GUI depicted in Figure 3-37. The features that are unique to this GUI are contained within the red dashed-line ovals, which are shown enlarged in Figure 3-38. To illustrate the use and capabilities of this GUI, we return to the original, essentially artifact-free data set considered in Section 2, and we have restored the complete set of Start and Stop markers.

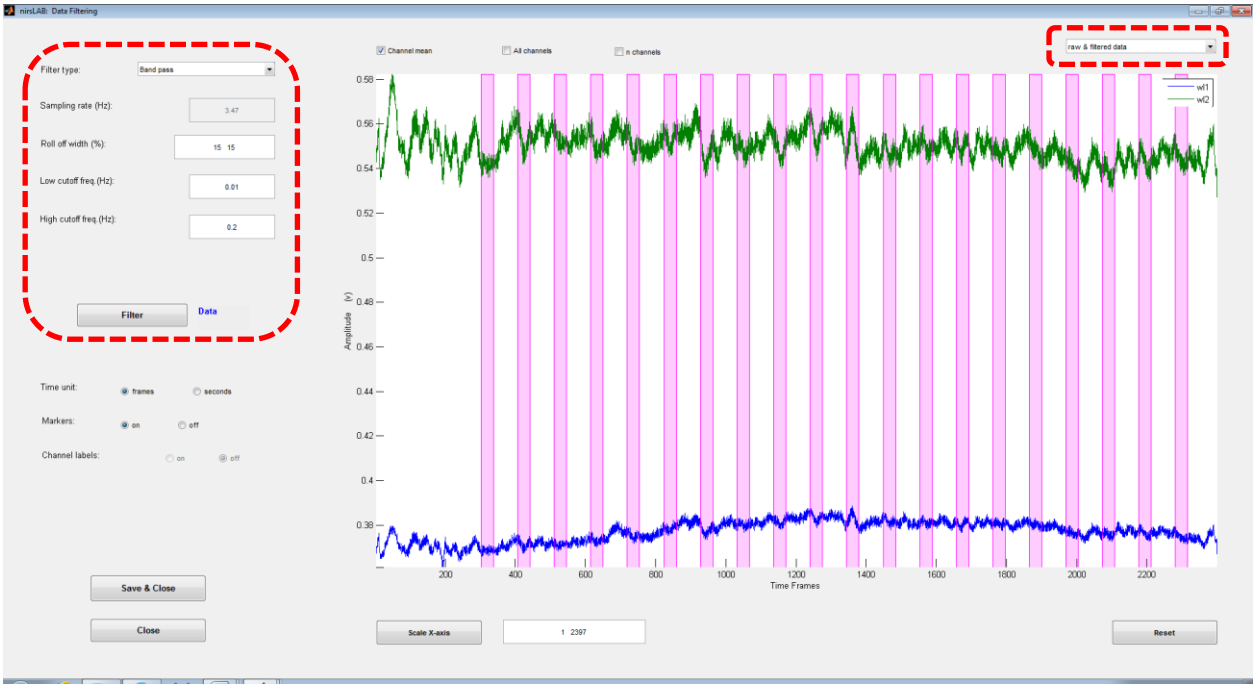


Figure 3-37. The *Apply Frequency filter* GUI, with its default display options selected.

The previous Sections of this chapter were largely concerned with the phenomena of artifacts and long-term drifts. While you might regard those as fundamentally different things, in another sense you can think of them as just two varieties a single property that time-series data might have: the data value can change over time in ways that are not related to the experimental paradigm, and these extraneous variations can interfere with your ability to accurately characterize the paradigm-related changes. It is merely convenient, in many cases, for you to think of artifacts and drifts as two different things, because the extraneous variations evolve over different time scales. The principle that underlies frequency filtering is that, just as you can delete features that you see in data in a localized time intervals, you can also remove fluctuations that are distributed over the entire measurement period but are localized in terms of their time scales.

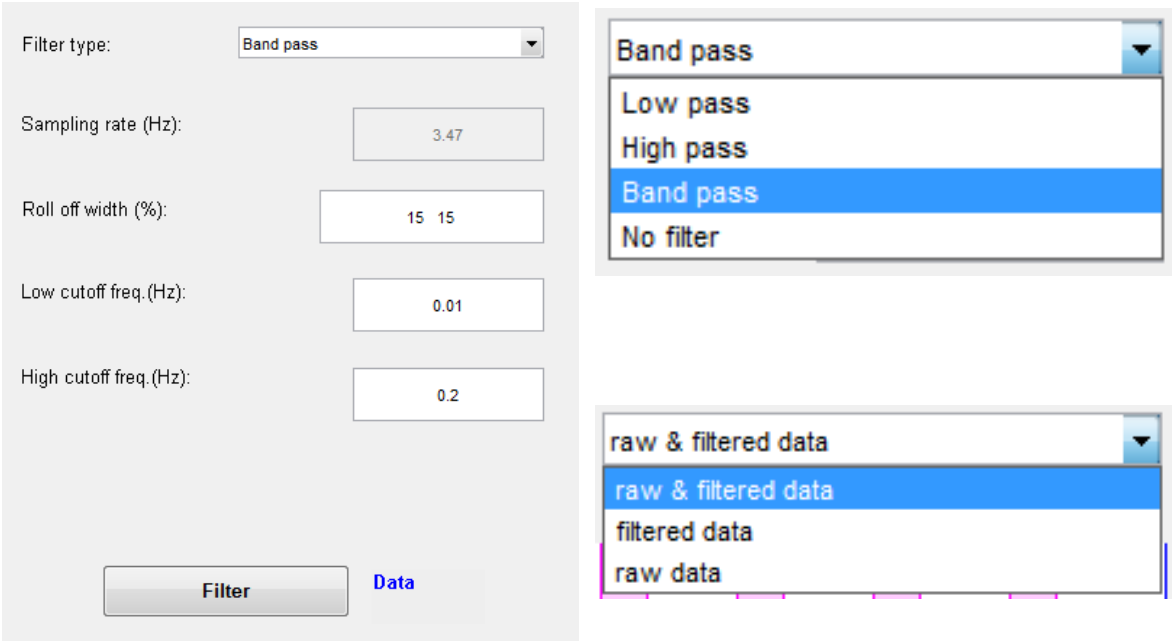


Figure 3-38. Detail view of the fields of the *Apply Frequency filter* GUI (Figure 3-37) that are used to design the filter (left), the items that are in the 'Filter type:' menu (right, top), and the items in the display-options menu (right, bottom).

The three basic types of frequency filter are:

- Low pass: A threshold frequency, or time scale is specified, and all fluctuations that evolve over more rapid time scales are deleted from the data time series. Phenomena such as noise (*e.g.*, the random variations that your imager would record if you were to turn all the light sources off) tend to occur at high frequencies. Consequently, low-pass filters are often used for de-noising purposes.
- High pass: A threshold frequency, or time scale is specified, and all fluctuations that evolve over less rapid time scales are deleted from the data time series. A long-term drift is a limiting case of a low-frequency fluctuation. Consequently, high-pass filters are often used for de-trending purposes.
- Band pass: It is convenient to think of this type as a low-pass filter and a high-pass filter combined into a single operation. Two threshold frequencies are specified, and both the very rapid and the very slow fluctuations are removed from the data. If the experimental events occur at a regular time interval, as in the demo data set considered here, then you select frequency thresholds that straddle the protocol-related frequency while excluding other fluctuations that are evolve on faster or slower time scales.

In Figure 3-38, you can see that there also is a fourth item, 'No filter', in the 'Filter type:' pull-down menu. You may wonder why you should bother to launch *Apply Frequency filter* at all if you don't

actually want to apply a frequency filter! One reason is that, as a practical formality, nirsLAB will not allow you to perform a *Hemodynamic States* computation (Chap. 4) until you first open and close the *Apply Frequency filter* GUI. We have incorporated this feature into nirsLAB in order to ensure that the absence of any frequency filtering is a deliberate choice and not a simple oversight.

The other user-definable filter properties (Figure 3-38) are:

- 'Roll off width:'. There is a theoretical possibility that, after you apply a frequency filter, you will notice a phenomenon called "ringing"[4] in your data time series. If it does occur, you can reduce its magnitude by entering larger values into the 'Roll off width:' field, and then re-applying the filter. We expect, however, that the default values will give you satisfactory results in most cases, especially if you remove discontinuities and spike artifacts (if any) before you apply the frequency filter.
- 'Low cutoff freq. (Hz):'. The threshold value that sets the time scale for long-term fluctuations (*e.g.*, drifts) that you want to remove from the data. With the default value of 0.01 Hz, any fluctuation that has 100 or more seconds per cycle will be deleted. Note that this number field will be grayed out if you select the 'Low pass' filter type, and the label will change to 'Cutoff freq. (Hz):' if you select the 'High pass' filter type.
- 'High cutoff freq. (Hz):'. The threshold value that sets the time scale for short-term fluctuations (*e.g.*, noise) that you want to remove from the data. With the default value of 0.2 Hz, any fluctuation that has 5 or fewer seconds per cycle will be deleted. Note that this number field will be grayed out if you select the 'High pass' filter type, and the label will change to 'Cutoff freq. (Hz):' if you select the 'Low pass' filter type.

After you specify the filter type, cutoff frequency or frequencies, and (optionally) roll-off width, click on the *Filter* button shown in Figure 3-38 to apply the filter. (If the number of measurement time frames is large, a noticeable amount of time may be required for the frequency-filtering computation. A pop-up window containing a progress bar will pop up on your screen, so you will know that the computation is ongoing and nirsLAB has not stalled or crashed.) With the default 'raw & filtered data' display-options menu item selected, the plot field will show the both the original time series (in gray) and the frequency-filtered one (in the original color). Alternatively, you can view only the original data or only the filtered data, by selecting the appropriate item from the pull-down menu.

If you want to change one or more filter parameters, you can simply specify the new values and click on *Filter* again. It is not necessary for you to first "undo" the effect of the previous filter computation(s). However, you may, if you want, restore the original data by selecting 'No filter' from the 'Filter type:' pull-down menu and clicking on the *Filter* button.

Examples of frequency filtering, for each of the three filter types, are shown in Figures 3-39 (band pass), 3-40 (low pass) and 3-41 (high pass). To facilitate viewing of the time series, the 'Markers: off' display option is selected.

To incorporate the filtering operations you have specified in *Apply Frequency filter* into the project-specific nirsInfo file, click on the *Save & Close* button near the lower-left corner of the GUI (see Figure 3-37). To exit from the GUI without implementing the filter, click on the *Close* button instead.

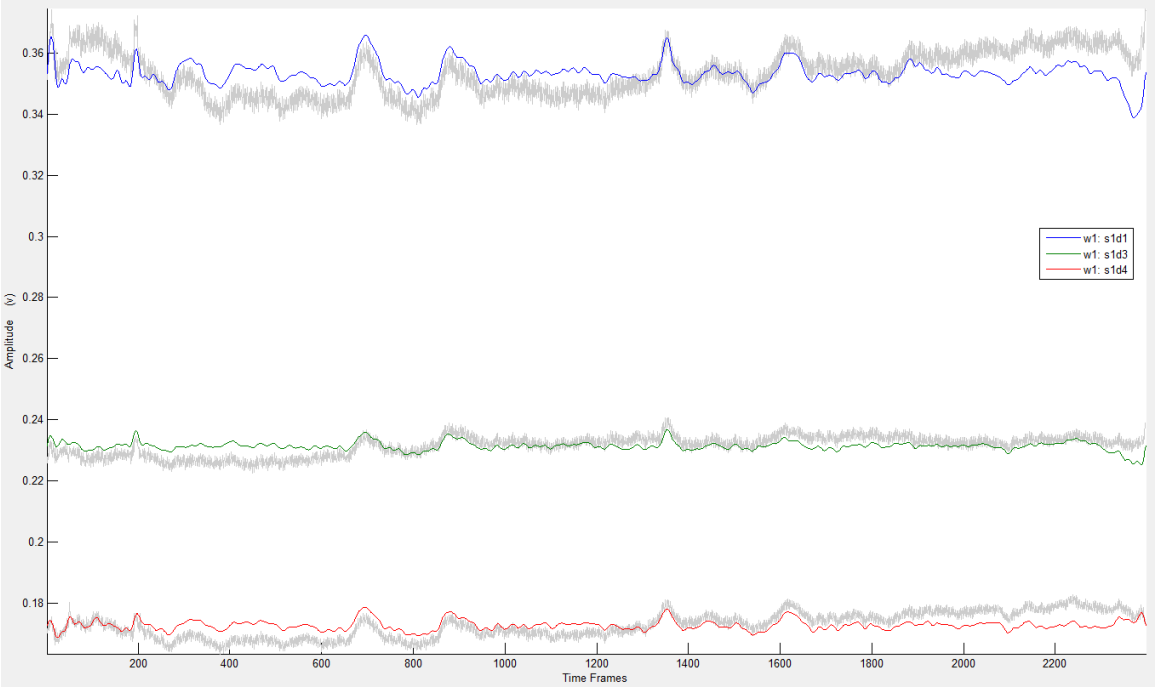


Figure 3-39. Example of the *Apply Frequency filter* GUI's plot window, illustrating the effect of a band pass filter (default cutoff frequencies and roll-offs) on time-series data.

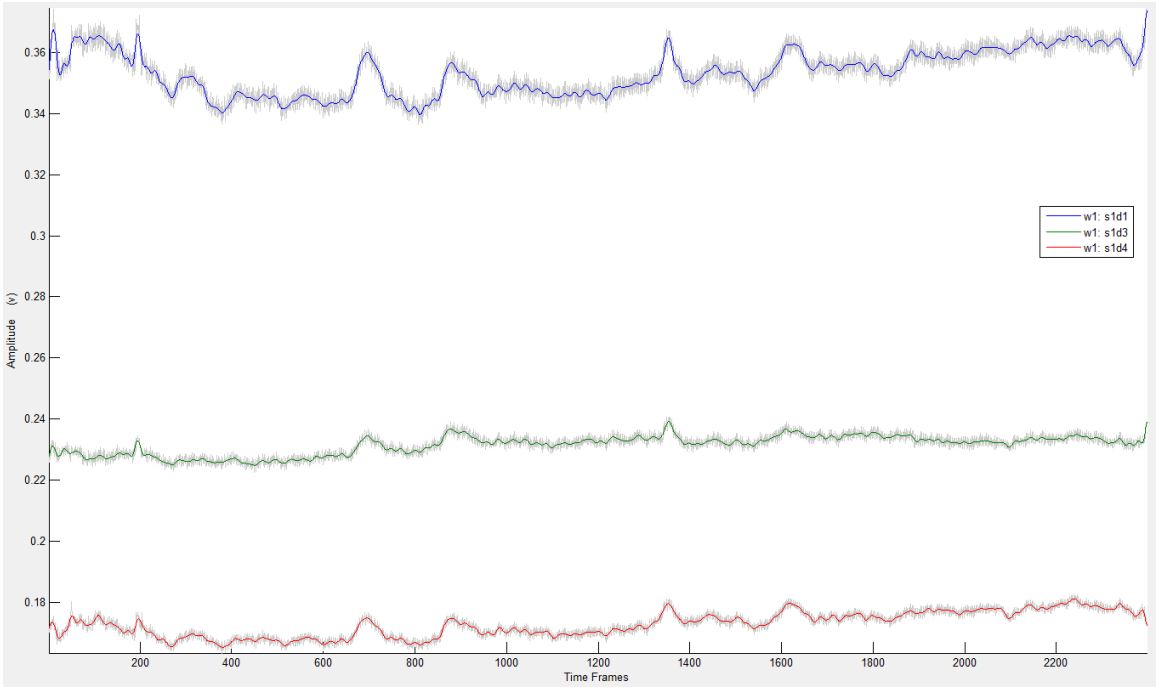


Figure 3-40. Example of the *Apply Frequency filter* GUI's plot window, illustrating the effect of a low pass filter (default cutoff frequency and roll-off) on time-series data.

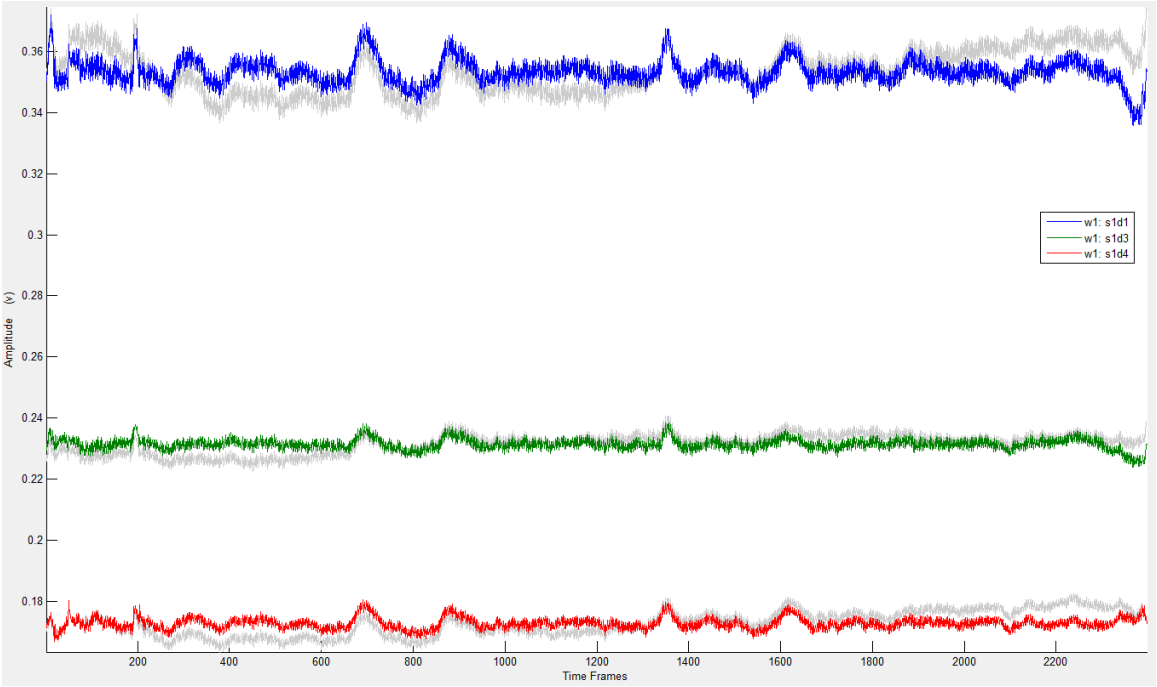


Figure 3-41. Example of the *Apply Frequency filter* GUI's plot window, illustrating the effect of a high pass filter (default cutoff frequency and roll-off) on time-series data.

6 References

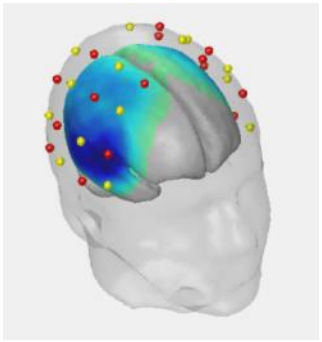
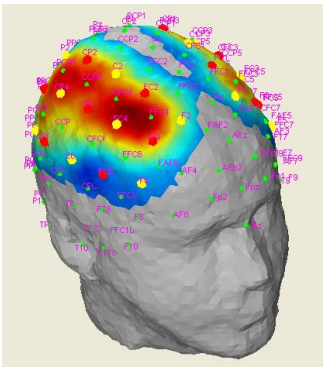
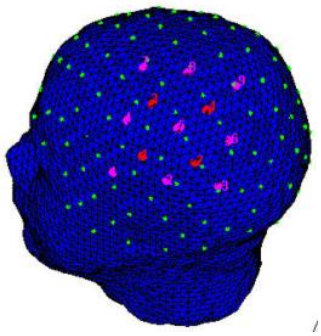
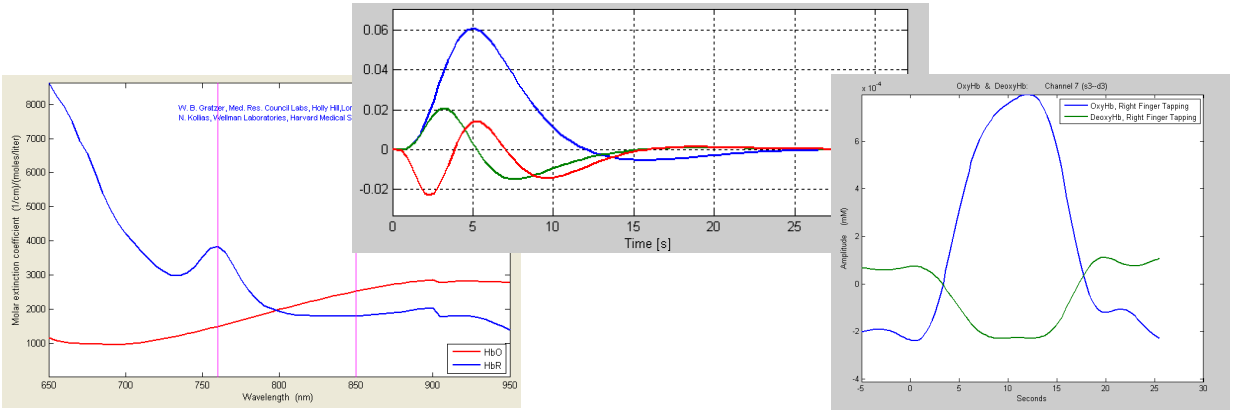
[1] T. Fekete, D. Rubin, J.M. Carlson, and L.R. Mujica-Parodi, "The NIRS Analysis Package: Noise Reduction and Statistical Inference," *PLoS ONE* **6**(9), e24322 (2011).

[2] I.W. Selesnick, H.L. Graber, D.S. Pfeil, and R.L. Barbour, "Simultaneous Low-Pass Filtering and Total Variation Denoising," *IEEE Transactions on Signal Processing* **62**(5), 1109-1924 (2014). Available for downloading from http://otg.downstate.edu/Publication/SelesnickTSP14.pdf.

[3] http://en.wikipedia.org/wiki/Imputation_%28statistics%29.

[4] http://en.wikipedia.org/wiki/Ringing_artifacts.

nirsLAB

Chapter 4: Hemodynamic States

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1 Introduction

The components in the **Hemodynamic States** portal of the **nirsLab** GUI, shown in Figure 4-1, allow you to compute the time series of hemodynamic states (*i.e.*, oxy-Hb, deoxy-Hb, tissue blood volume, HbO_2 saturation) from the filtered data produced by the preprocessing utility (see Data Preprocessing, Chapter 3) by use of the Beer-Lambert Law. These components consist of:

- The **Set** parameters button
- The **Compute** Hemodynamic states button

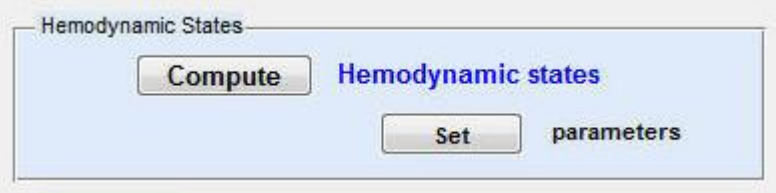


Figure 4-1: Portal for Hemodynamic States

2 Setting Parameter Values

Setting parameters is the first step you need to take in order to compute the hemodynamic states.

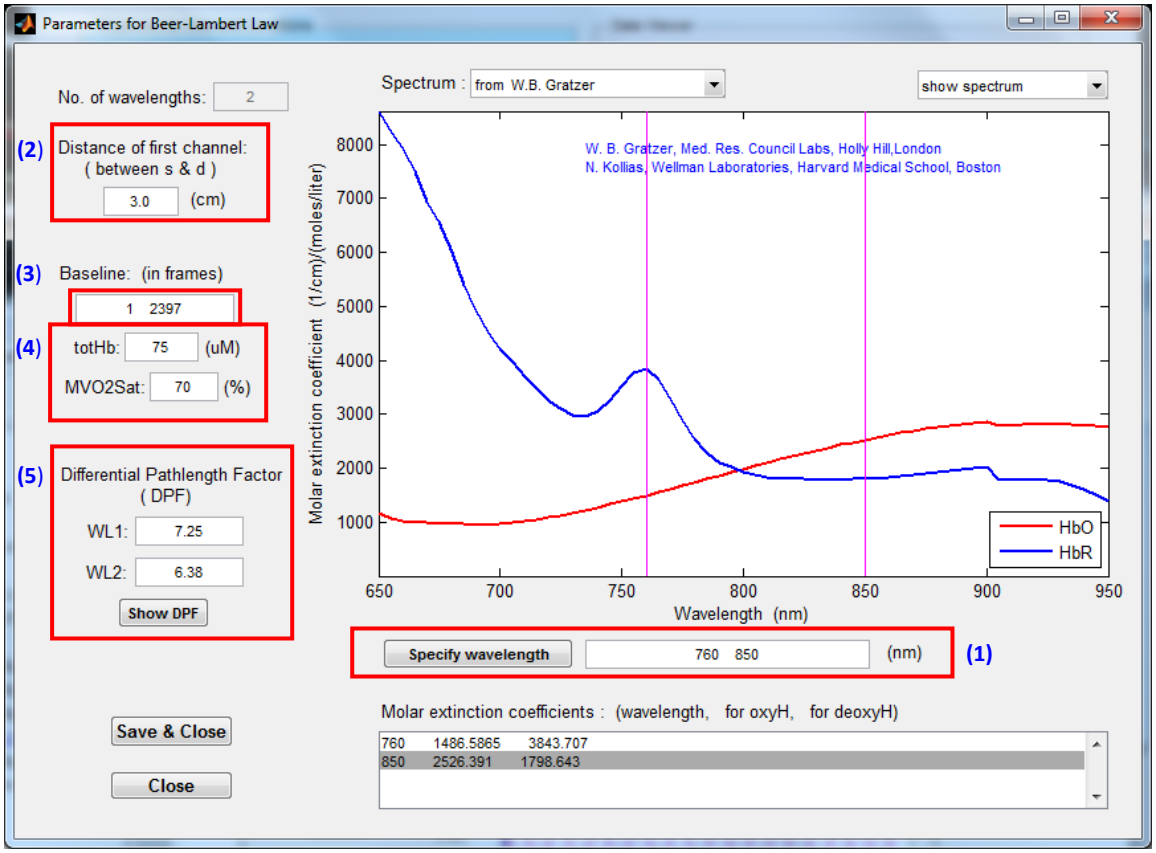


Figure 4-2. Parameter settings for Beer-Lambert Law

Click the **Set** parameters button in the **Hemodynamic States** portal to open a new GUI named 'Parameters for Beer-Lambert Law', shown in Figure 4-2, that will allow you to either accept or change the default parameters. Highlighted in red are five parameter fields;

- Specify wavelengths (1)
- Distance of first channel (2)
- Baseline (3)
- Background tissue values (4)
- Differential pathlength factor (5)

To specify wavelengths, simply enter the value of the peak illumination wavelengths used for your instrument in field (1). For NIRSport and NIRScout systems, the correct values are 760 and 850 nm, for DYNOT systems, the correct values are 760 and 830 nm. Alternatively, wavelength selection can be made graphically by clicking on the 'Specify wavelength' button. This will enable a set of crosshairs that you can move by using the mouse.

Because there are some differences in the reported extinction coefficients for hemoglobin in the literature, a pull down menu located at the top of the GUI is provided so that users can select from spectra published by three commonly referenced reports as shown in Figure 4-3**.**

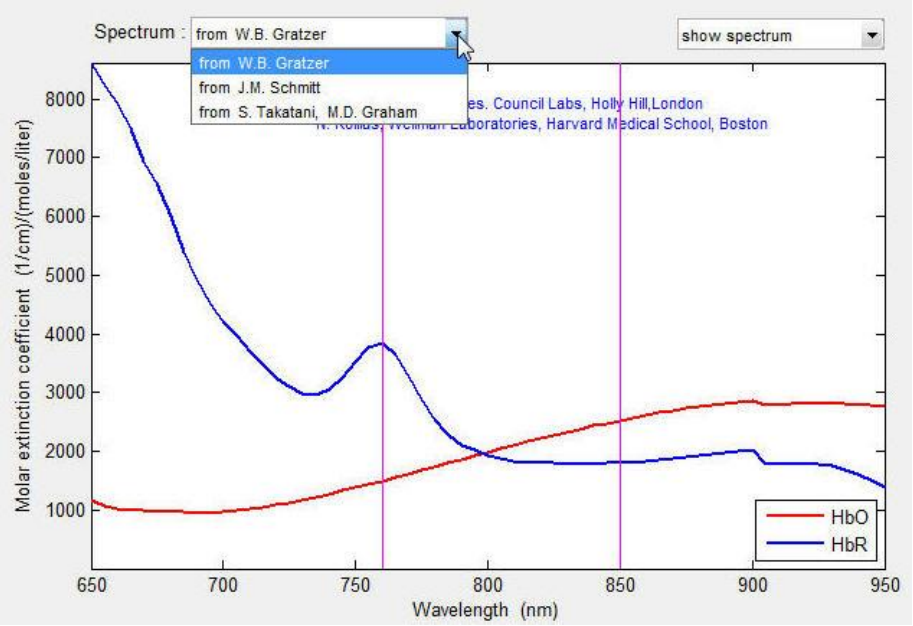


Figure 4-3. Selected spectra of reported hemoglobin values.

The 'Distance of first channel', (2), refers to the physical distance in cm between the source and detector for channel 1 specified using the Probes Setup portal described in **Chapter 7**. The default value is 3 cm. This value is then used to scale all other channels that have been specified. Should this distance associated with channel 1 differ significantly from the default setting, users should carefully measure the actual distance for each subject.

The 'Baseline" field, (3), refers to the time period that corresponds to a baseline wherein subjects are typically resting quietly. The default setting is set to the full time course of the data set. Depending on the experimental conditions, users may wish to restrict this to the period having shorter duration. To help you to specify the baseline, the parameter GUI provides a way to view the spatial mean time series of your filtered raw data and the event markers in the axes of the GUI. The following figures show an example how to view the data and event markers in the GUI. Clicking the pull-down menu in upper right corner of the GUI and selecting the option "show raw data (mean)", you can see the data and event markers in the axes of the GUI, as shown in Figure 4-4.

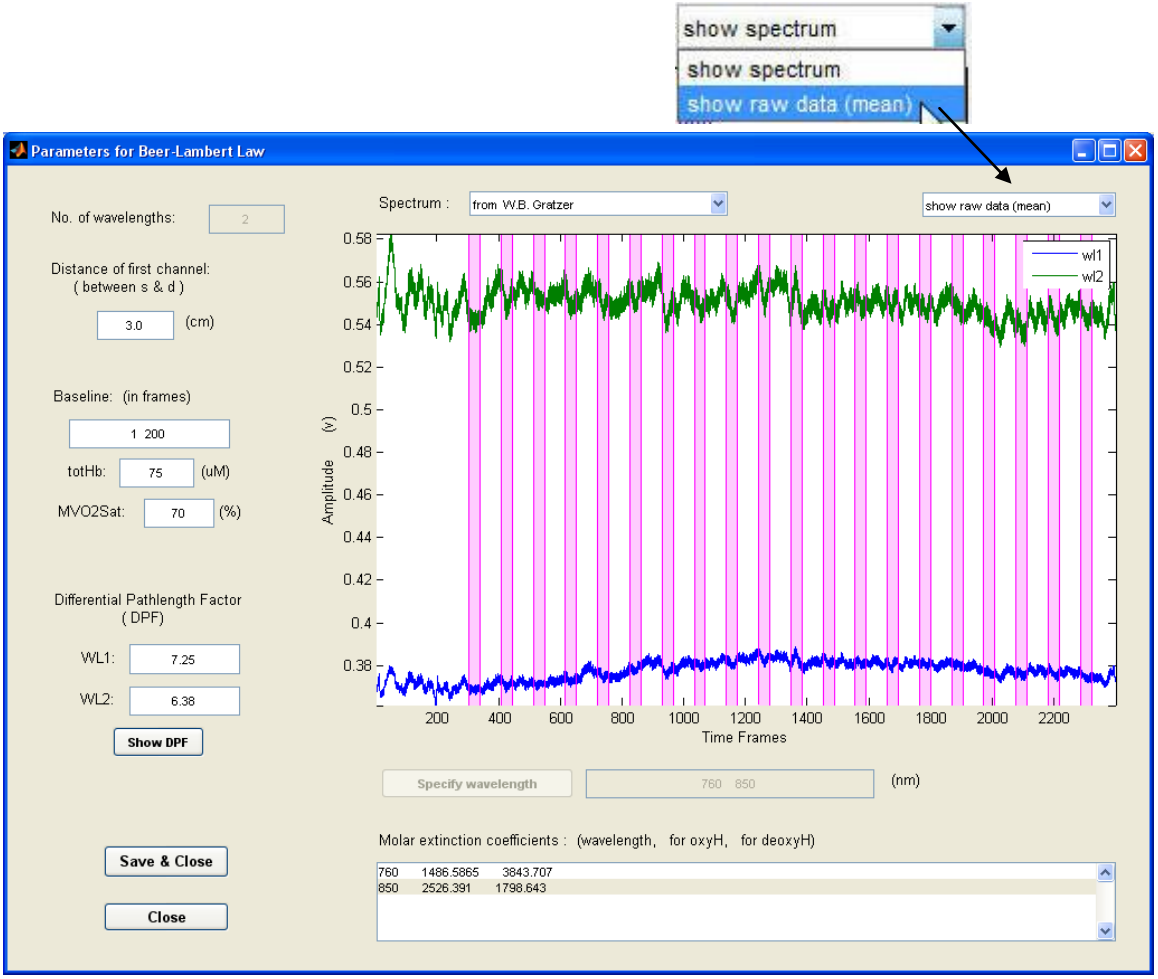


Figure 4-4 . Spatial mean display with event markers

Listed below the Baseline field are two additional fields that correspond to estimated values of the background hemoglobin content in tissue (default value, 75 uM), and the Mean Venous O_2Saturation value (default value, 70%, MVO2Sat), (4).

Yet another parameter setting is the Differential Pathlength Factor (DPF) that takes into account the additional average distance light travels due to scattering beyond the linear distance between a source

and receiver. He we have selected a values representative of reports described in the literature [Essenpreis et al. Applied Optics 32, 418-425, 1993, M Kohl, Phys. Med Biol, 43, 1998, 1771-1782, H. Zhao, et al. Phys. Med. Biol, 47, 2075-2993, 2002]. It deserves noting that the true value will depend on details of head shape, skull thickness, and properties of underlying tissues.

After all parameters are specified, you must save the new parameter sets, otherwise you have to set the parameters again when you compute the hemodynamic states. Just clicking the **Save & Close** button in lower left corner of the parameter GUI, as shown in Figure 4-5, the newly specified parameters will be automatically saved into a nirsInfo file located in the **nirsLab** working folder.

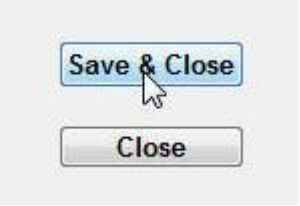


Figure 4-5

3 Computing Hemodynamic States

After you finish setting and saving the parameters, you can compute the time series of hemodynamic states from the filtered raw data by clicking the **Compute** button prior to the words "Hemodynamic states" in the Hemodynamic States portal as shown in Figure 4-6.

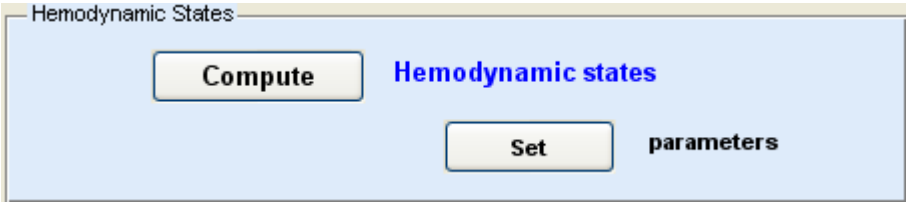
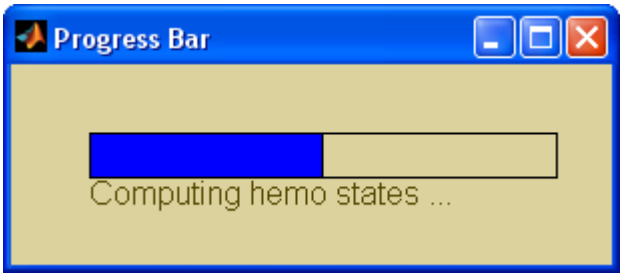


Figure 4-6. Click 'Compute' to enable computation of hemodynamic states using information given in (1) – (5).

During the process, progress bars appear to show how calculations are proceeding.



When the computing is done, the computed hemodynamic states will be automatically saved in MATLAB binary format in the **nirsLab** working folder. Then you can view the time series and map them onto head or brain surface by using the **nirsLab** data-viewing functions (see Data Viewing, Chapter 5). And you can also export the hemoglobin time series, if you want, as a text file for some future uses by use of the **nirsLab** data-exporting tool (see Data exporting, Chapter 8).

4 New Files Created

Following the above steps a new binary file is created having the syntax of, h_*filename*.dat, in the Detectors folder that contains the newly computed values for oxyhemoglobin and deoxyhemoglobin for each channel specified using the Probes Setup utility. Also updated, is information pertaining to the selected parameter setting saved in the *filename*_nirsInfo.mat file. Export of the hemoglobin files is possible using the 'Data Export' portal described in Chapter 8.

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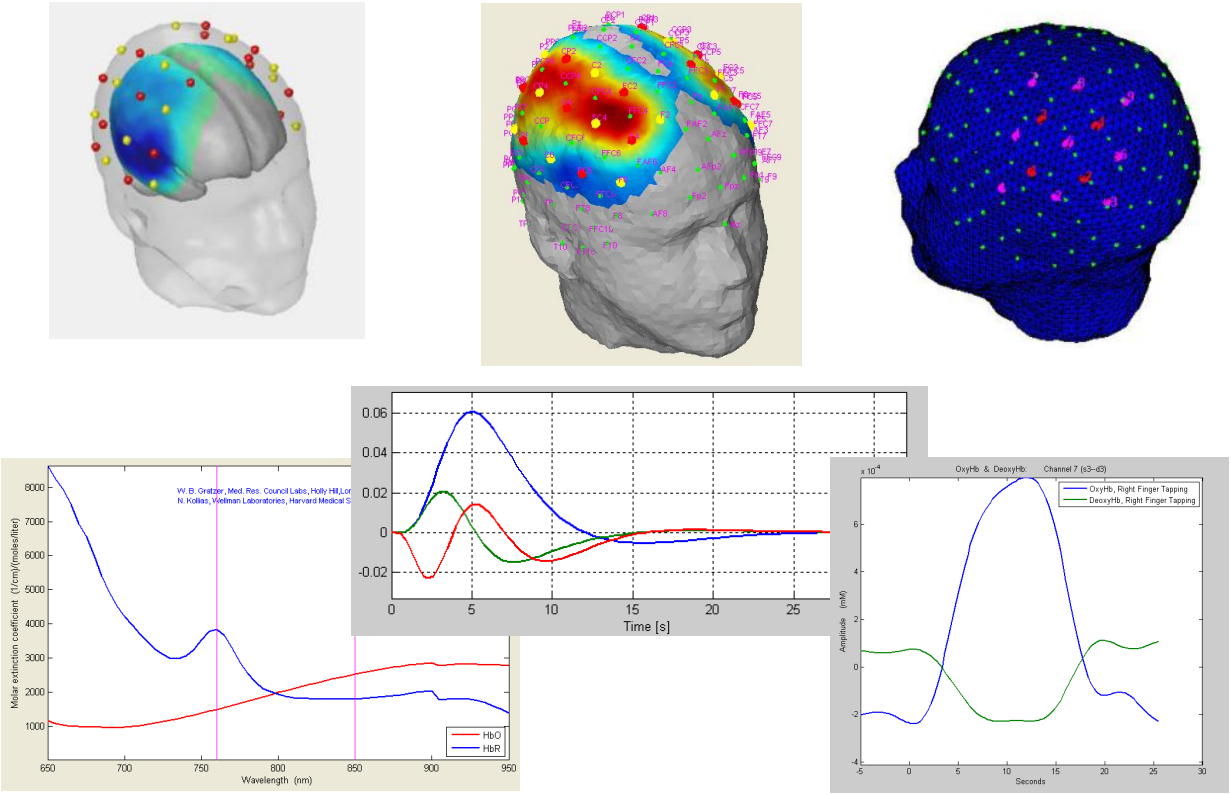
nirsLAB



Chapter 5: Data Viewing

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1 Introduction

The Data Viewing module provides a variety of visualization tools for plotting individual raw and processed channel responses, in either the time or frequency domain, as well as several anatomy-based mapping resources that explore time-varying and event-averaged responses recorded by the sensing array. Various zoom, rotate, and montage display features are also available to assist in data examination. Under construction is a meta-data viewer ('Data processing info'), which will record the history of parameter specifications and identify where intermediate saved files are located.

An additional functionality provided by this portal is the ability to explore responses of all source-detector pairs, not just the ones defined in the probe layout. Because variability in probe placement can result in some channels having excessive noise, an additional editing feature is included that supports exclusion of user-specified channels from further analysis and mapping.

Figure 5-1 shows the GUI to access features supported by the *Data Viewer* portal. You can use these functions to plot detector-channel time series, to map hemodynamic images onto a scalp or a brain cortex surface, and to view recorded information pertaining to the measurement and to all data processing operations performed so far, respectively.

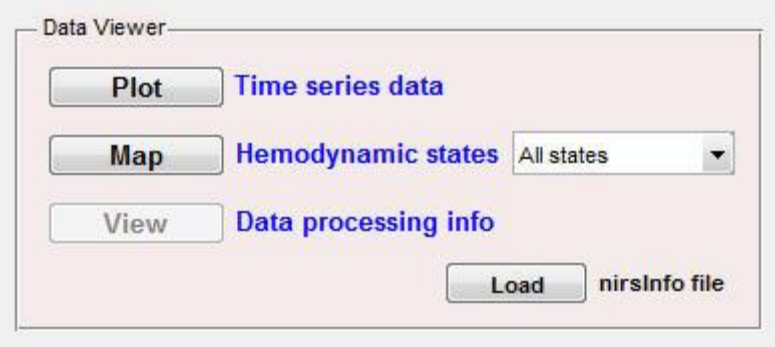


Figure 5-1. Data Viewer portal for exploring time- and position-dependent channel responses.

If you have completed the processing steps outlined in Chapters 3 (Data Preprocessing) and 4 (Hemodynamic States) and wish to display information in the currently loaded data set, you can simply click on the *Plot*, *Map* or *View* buttons in the *Data Viewer* portal. If you want to view data that was generated earlier in the current nirsLAB session, or in a previous session, you will need to first load the project-specific nirsInfo file by clicking the *Load nirsInfo file* button seen in Figure 5-1. This will open the browser window shown in Figure 5-2, which you will use to navigate to the folder where the nirsInfo file you wish to access is stored. Highlight the file and click on the *Open* button (lower right corner of the navigator window).

The following sections will show you how to use these three modules to view the different nirsLab-based data sets and data processing information.

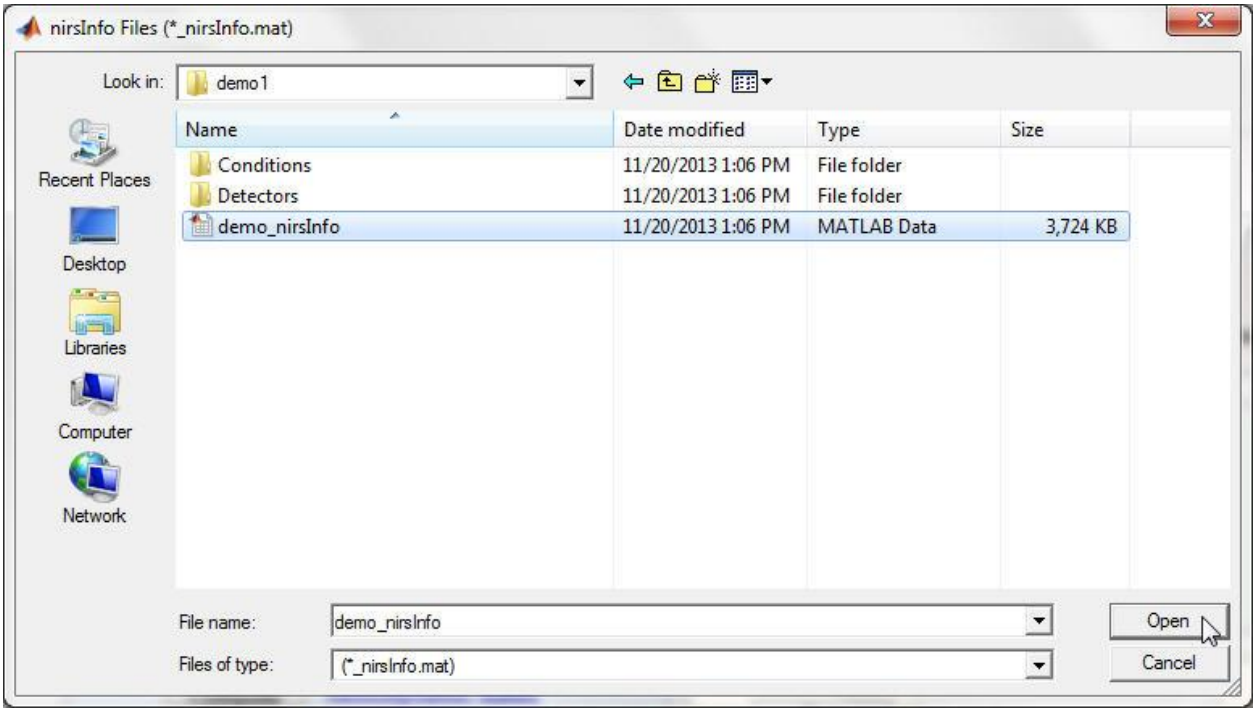


Figure 5-2. Browser window for selecting a nirsInfo file.

2 Plot Time Series Data

Pressing the *Plot Time series data* button seen in Figure 5-1 brings up a new GUI named 'Time Series Data Viewer', shown in Figure 5-3, which allows you to display, edit and export the detector-channel/nirs channel time series. (Note that the project name also is displayed in the GUI title bar.)

The capabilities provided by the viewer are:

- Display of time series for an individual detector channel, and its power spectral density (PSD) vs. frequency.
- Simultaneous display of multiple time series for a single channel, and their PSDs. This allows comparisons of different experimental variables (e.g., edited detector-channel time series at two measurement wavelengths, or three states of hemoglobin [Hb]).
- Display of block-averaged time series for all experimental conditions and all channels defined in the probe setup (Chap. 7), for a single specified variable.
- Stacked display of time series for all detector channels, for a single specified variable.
- Colored contour-surface display of time series for all detector channels/nirs channels, for a single specified variable.

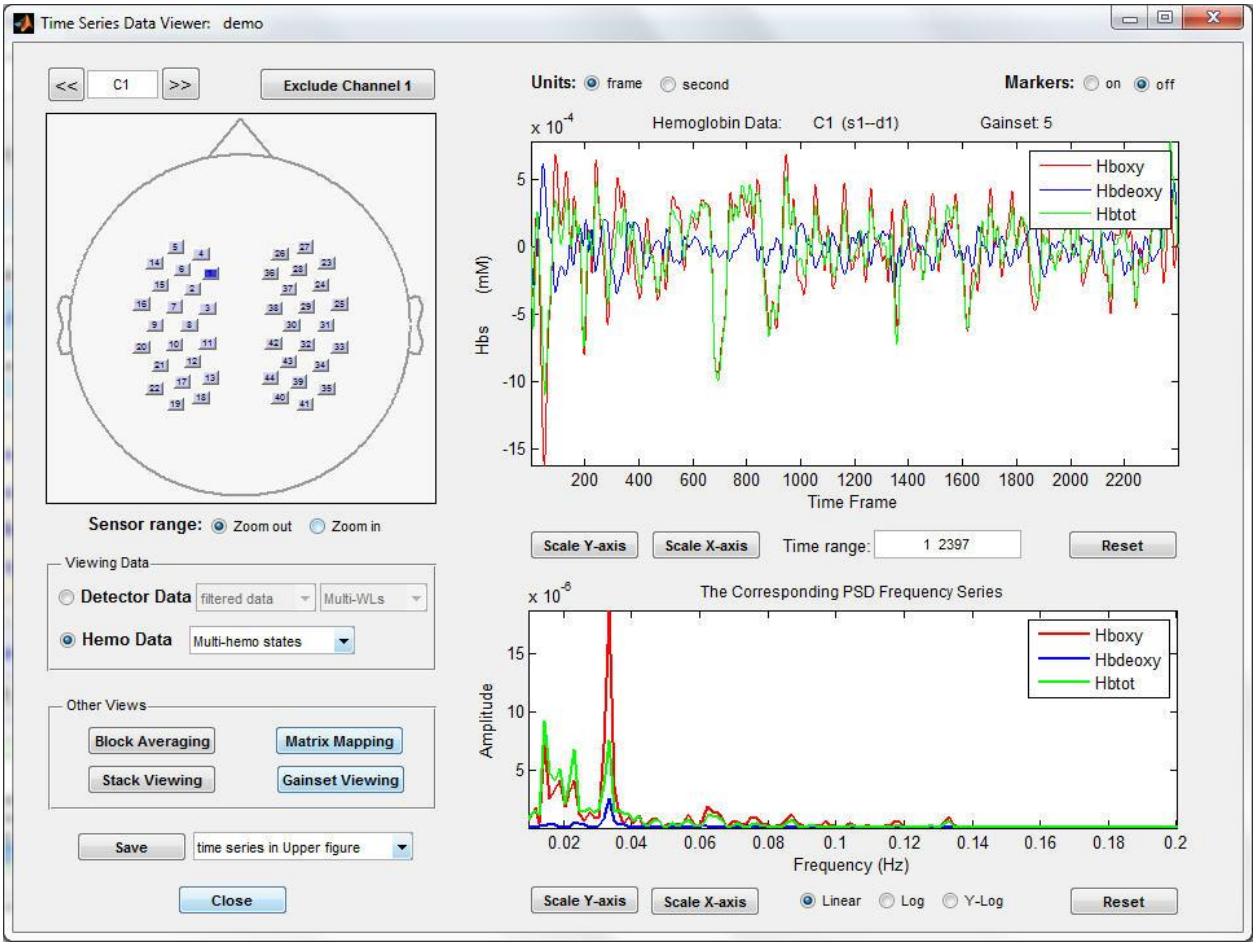


Figure 5-3. Plotting time series data and the *Time Series Data Viewer* GUI, with its default display options selected.

In addition, the module offers control functions that allow you to easily:

- Switch to a different display variable (e.g., from raw detector data to oxy-Hb and deoxy-Hb concentration, to HbO2 saturation, to edited and filtered time series);
- Select which specific channel to display;
- Specify the time interval for the currently displayed variable as well as for its PSD estimate;
- Change the scales on all plots (*i.e.*, zoom in/out);
- Reset the plots to their default display settings; save a user-specified time series.

2.1 Selecting a specific detector / hemoglobin data set

The components of the *Viewing Data* module of the *Data Viewer* GUI, which is highlighted in Figure 5-4, allow you to select a specific data type for viewing. There are two data types you can select through radio buttons: 'Detector Data' and 'Hemoglobin Data'.

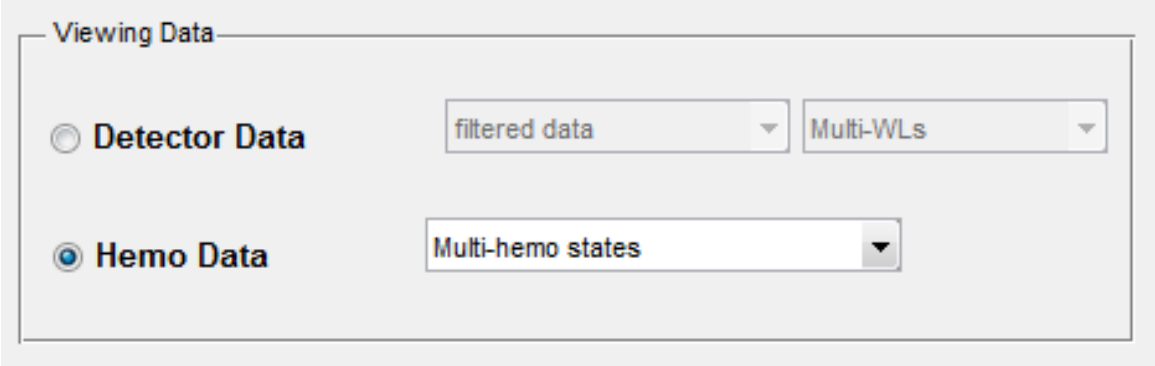


Figure 5-4. Detail view of the *Viewing Data* components of the *Time Series Data Viewer* GUI.

There are two data types you can select through radio buttons: 'Detector Data' and 'Hemo Data'.

2.1.1 Detector Data

By clicking the 'Detector Data' radio button (this is the default case), you can select the detector time series data for viewing. After the radio button is chosen, two pull-down menus following the button will be enabled. As shown in Figure 5-5, clicking on the first pull-down menu, you can select one of three detector data sets: raw data, edited data and filtered data to display. Using the second pull-down menu, you can specify the single wavelength data or multiple-wavelengths data for viewing.

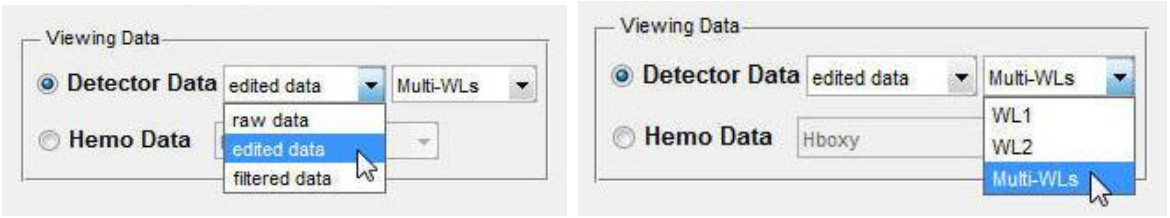


Figure 5-5. Data selection pull-down menus.

2.1.2 Hemo Data

Clicking the Hemo Data radio button (this is the default case), you can select the hemoglobin time series data for viewing. After the radio button is chosen, a pull-down menus following the button will be enabled. As shown in Figure 5-6, the pull-down menu allows you to select a specific hemoglobin-state-dependent data for viewing. As an example, here, the multiple-hemoglobin states option is selected (the HbO2Sat variable is not included in the option), and the Hboxy, Hbdeoxy and Hbtot hemoglobin data sets are viewed simultaneously.

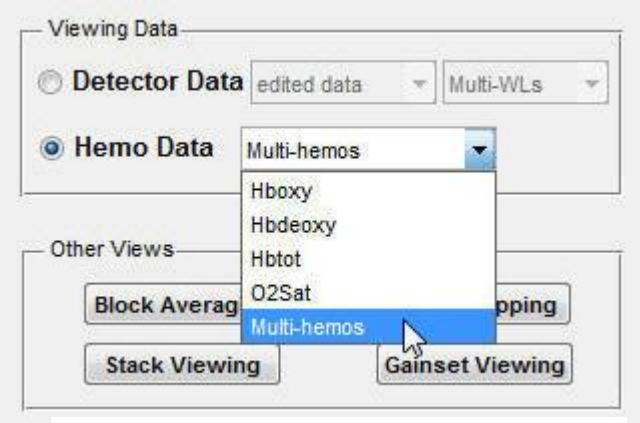


Figure 5-6. Selection of hemoglobin state.

2.2 Selecting a specific source-detector / nirs channel

As identified in Chapter 7, the viewing formats for probe layouts corresponding to the *source-detector* channels and *nirs* channels are similar but not identical. Illustrated in Figure 5-7 are the corresponding probe layouts for the demo data set obtained from a finger tapping study. Shown in the upper left is layout corresponding to the source-detector array; upper right for the selected nirs-channels representing positions located between optode array elements. Below this is an expanded view of these obtained by clicking on the 'Zoom in' button located below the displays.

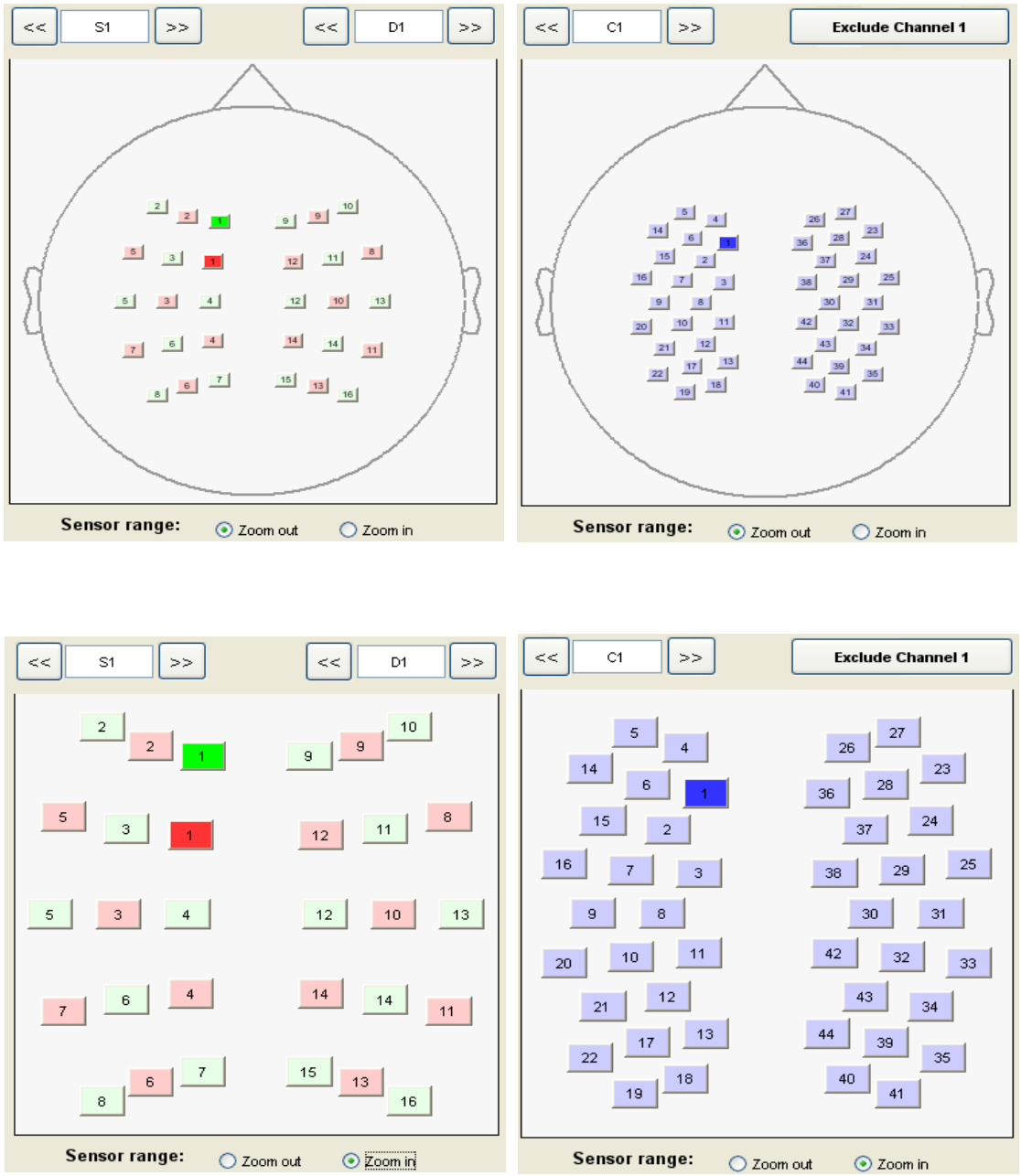


Figure 5-7. Display options for viewing topographic layout.

2.2.1 Select Source-Detector Channels

There are three ways to select a specific source-detector channel for raw data sets:

1. Directly type the source and detector numbers in the source and detector text fields. For example, if you want to select the source2-detector5 channel, as shown in Figure 5-8 , type

'S2' in the source text field and 'D5' in detector text field. Once entered, the (s2-d5) source-detector channel is immediately selected and the respective buttons are automatically highlighted.

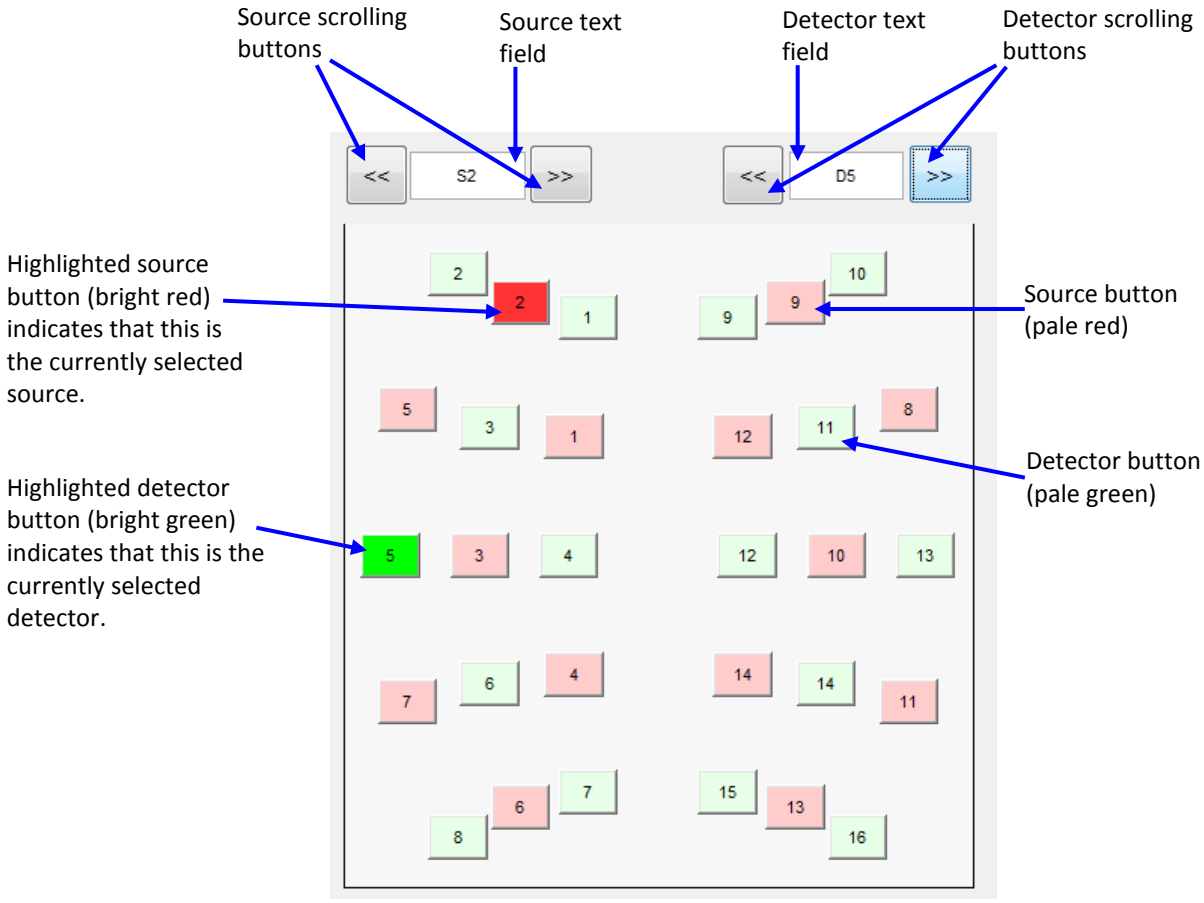

Source scrolling buttons
Source text field
Detector text field
Detector scrolling buttons
<<
S2
>>
<<
D5
>>
Highlighted source button (bright red) indicates that this is the currently selected source.
Source button (pale red)
Highlighted detector button (bright green) indicates that this is the currently selected detector.
Detector button (pale green)

Figure 5-8. Selecting a source-detector channel.

2. Use the source scrolling buttons "<<" and ">>" to scroll through the sources, and the detector scrolling buttons "<<" and ">>" to scroll through the detectors. The selected source and detector buttons will be automatically highlighted during your scrolling, and the source and detector text fields will be also automatically updated during the scrolling.

3. Directly click on the source and detector buttons to select the source-detector channel. The clicked buttons will be automatically highlighted, and the source and detector text fields will be also automatically updated.

2.2.2 Select nirs channels

Similar to the specification of source-detector channels, there are three ways to select a specific nirs channel for edited data, filtered data and hemoglobin data sets:

1. Directly type the nirs channel numbers in the nirs channel text fields. For example, as shown in Figure 5-9, if you want to select the nirs channel 7 for viewing, type 'C7' in the nirs channel text field. Once entered, nirs channel 7 is immediately selected and its corresponding channel button is automatically highlighted in dark blue.

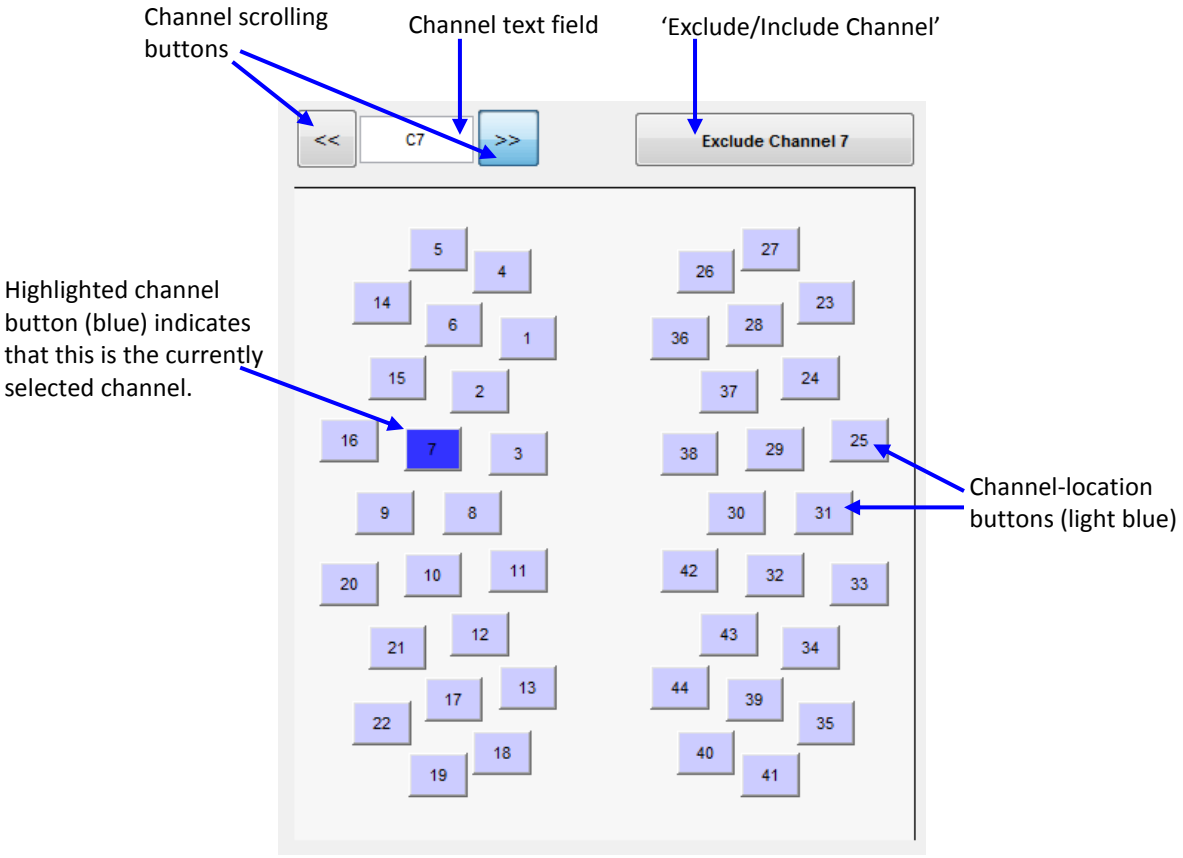


Figure 5-9. Selecting a channel from the set defined during probe setup.

2. Use the channel scrolling buttons "<<" and ">>" to scroll through the nirs channels. The selected nirs channel button will be automatically highlighted in dark blue during your scrolling, and the nirs channel text fields will be also automatically updated during the scrolling.

3. Directly click on the nirs channel button to select the nirs channel. The clicked button will be automatically highlighted in dark blue, and the nirs channel text fields will be also automatically updated.

2.3 Viewing selected time series data sets

As shown in Figure 5-10, the components in highlighted upper right corner of the Data Viewer GUI allow you to view and edit the time series data sets you have selected.

Figure 5-10. Detail view of the time-series plot window and associated user-control features in the *Time Series Data Viewer* GUI (Figure 5-3).

These components consist of:

axes: for plotting the specified time series data sets;
two **Units** radio buttons: for changing time units (x-labels in the axes);
two **Markers** radio buttons: for turn on or off the event markers in the axes;
Scale Y-axis button: for re-scaling the amplitude;
Scale X-axis button: for changing the plot time interval by using mouse;
Time range text field: for changing the plot time interval by typing the interval;
Reset button: for re-setting the plotting data sets back to original data sets.

It should be pointed out that the title of the axes indicates the plotting data type, channel and the gain setting of the channel. For example, the title of the axes in above figure shows that the plotting data is edited data, the data channel is the 7th nirs channel, and the gain setting of the channel is 5.

2.3.1 Change time units

Using the two unit radio buttons: **frame** and **second** in upper left corner of the plot, you can easily switch time units between frame and second. As shown in Figure 5-11, when you click on the second radio button, the time units of x-axis and the time range text field are immediately changed to 'Second'.

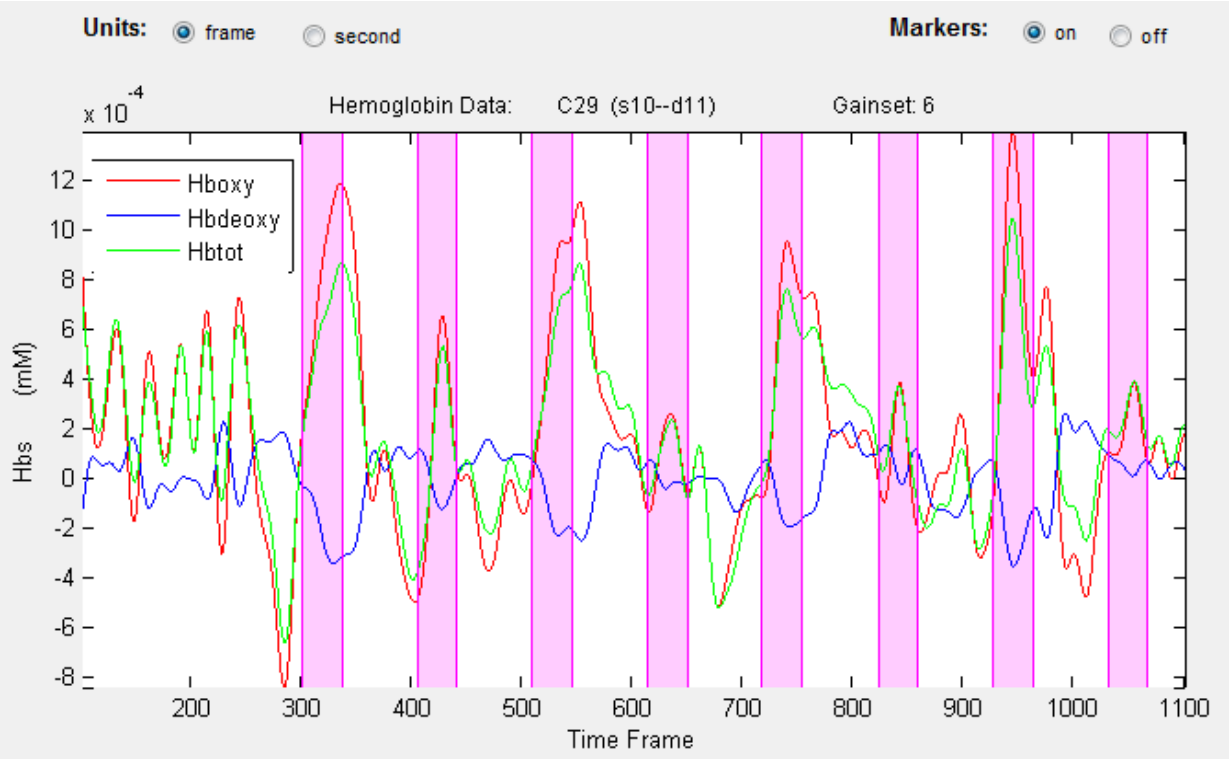


Figure 5-11. The same time series as in Figure 5-10, but with 'frame' selected as the time unit.

2.3.2 Plot event markers on axes

If you want to plot the event markers on the axes, just click the **on** radio button in upper right corner, as shown in Figure 5-12, the markers are immediately plotted on the axes.

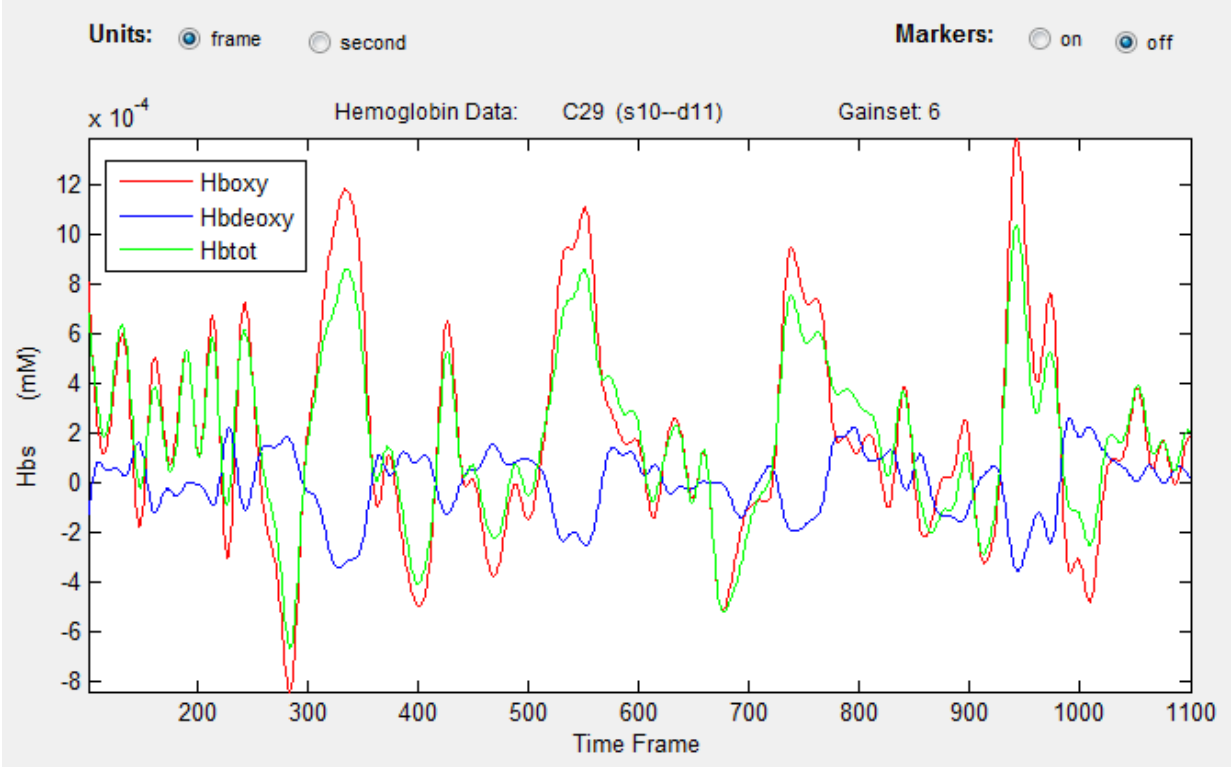


Figure 5-12. The same time series as in Figure 5-10, but with the event-marker display turned off.

2.3.3 Re-scale the amplitude

You can rescale the vertical axes, by using the **Scale Y-Axis** buttons. By default, each data channel's time series is scaled to its own minimum and maximum values. In contrast, using a **Scale Y-Axis** button will apply a user-defined scale range to all the channel-based time series plots in the specified data set. Shown in Figure 5-13, 5-14 and 5-15 are examples of using the scaling function for rescaling the amplitude.

***Step 1*:** Click the **Scale Y-Axis** button to open a text field window as shown below:

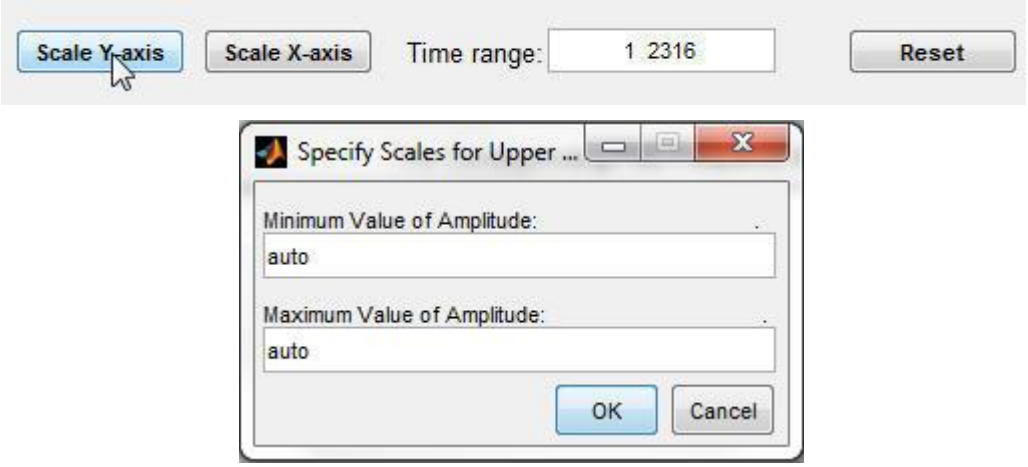


Figure 5-13. Rescaling the data amplitude.

***Step 2*:** Enter the desired minimum and maximum values for the display range of the vertical axis. For example:

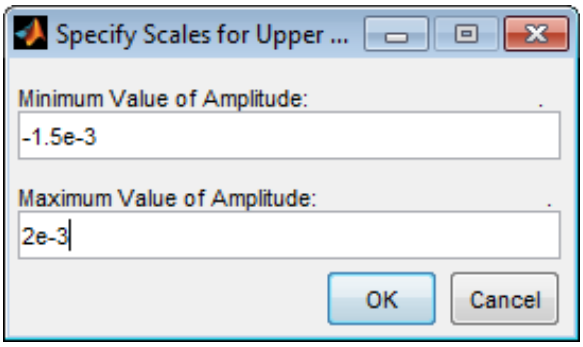


Figure 5-14. An example of rescaling the data amplitude.

***Step 3*:** Click the **OK** button to close the text field window. You will see an updated plot, with the new vertical scale limits:

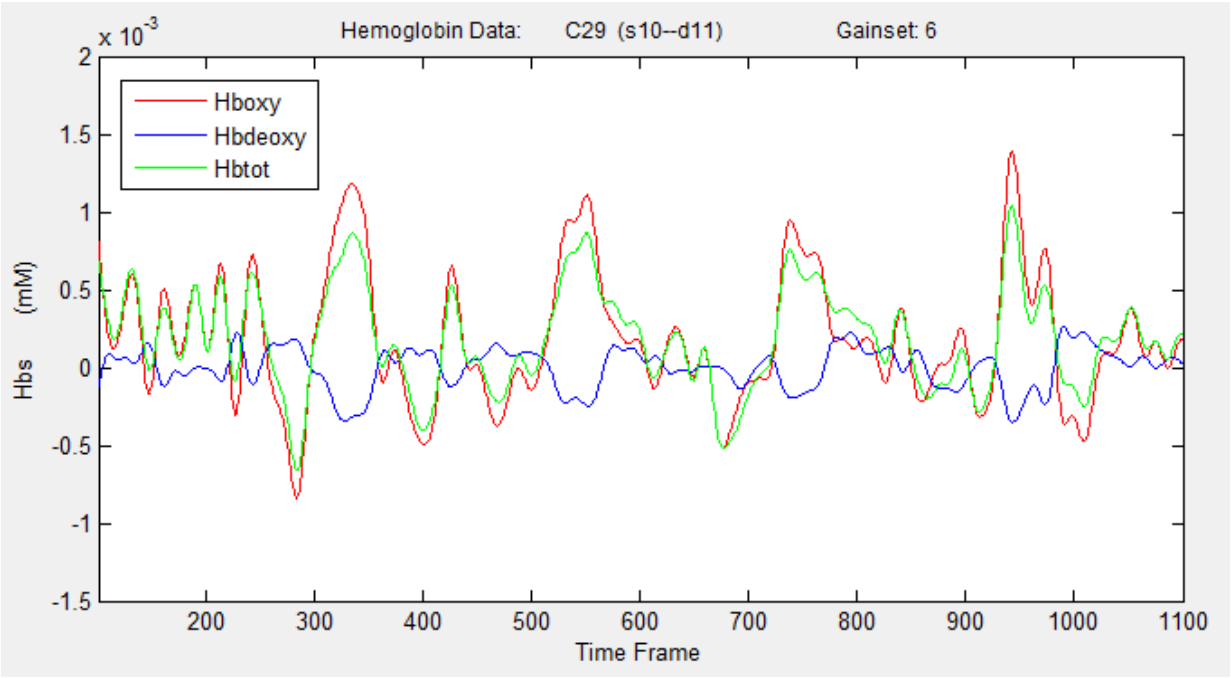


Figure 5-15. The same time series as in Figure 5-12, after adjusting the y-axis display range as depicted in Figure 5-14. (Note that you can adjust the location of the legend by simply "dragging" it with the mouse.)

***Note*:** You can reset the minimum and maximum values of the vertical-scale range to their default values by typing "auto" in the corresponding text fields, as shown in Figure 5-16.

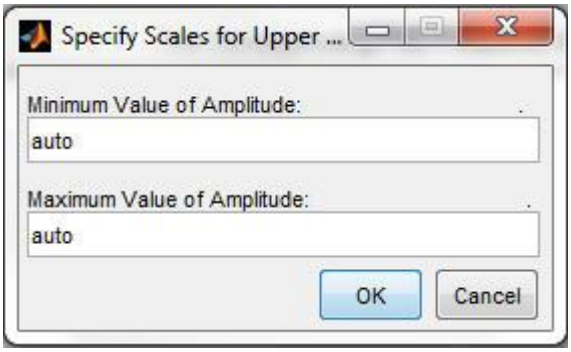


Figure 5-16. Reset the amplitude scaling into default values.

2.3.4 Adjusting the x-axis Display Range

By default, the entire data time series for the selected channel is displayed in the plot window. (For the exemplary data shown in Figures 5-10, 5-11, 5-12 and 5-15, we have intentionally modified the x-axis display range, in order to make it more apparent to visual inspection that there is a strong correlation between the finger-tapping events and the associated hemodynamic responses.) Two methods for adjusting the x-axis display range – the same methods that are described in Chap. 2, Section 4.2 – are provided by nirsLAB.

- Directly type the starting and ending times for the interval that you want to delete into the Time range: number field (Figure 5-13, top).
- Click on the Scale X-axis button (Figure 5-13, top) to activate plot-window crosshairs, which you will then use to select the starting and ending times by clicking on them.

2.3.5 Resetting the Plot Window Display Ranges

Click on the **Reset** button shown at the bottom right of Figure 5-10 in order to restore the display ranges for both axes to their default settings.

2.4 Viewing power spectral density (PSD) of selected time series data sets

As shown in Figure 5-17, the components in highlighted lower right corner of the Data Viewer GUI allow you to view and edit the power spectral density (PSD) of the time series data sets you have selected. These components consist of:

axes: for plotting the PSD *vs.* frequency;
Scale Y-axis button: for re-scaling amplitude;
Scale X-axis button: for changing the plot frequency interval by using mouse;
three radio buttons: for setting axes scale type;
Reset button: for re-setting the plotting data sets back to original data sets.

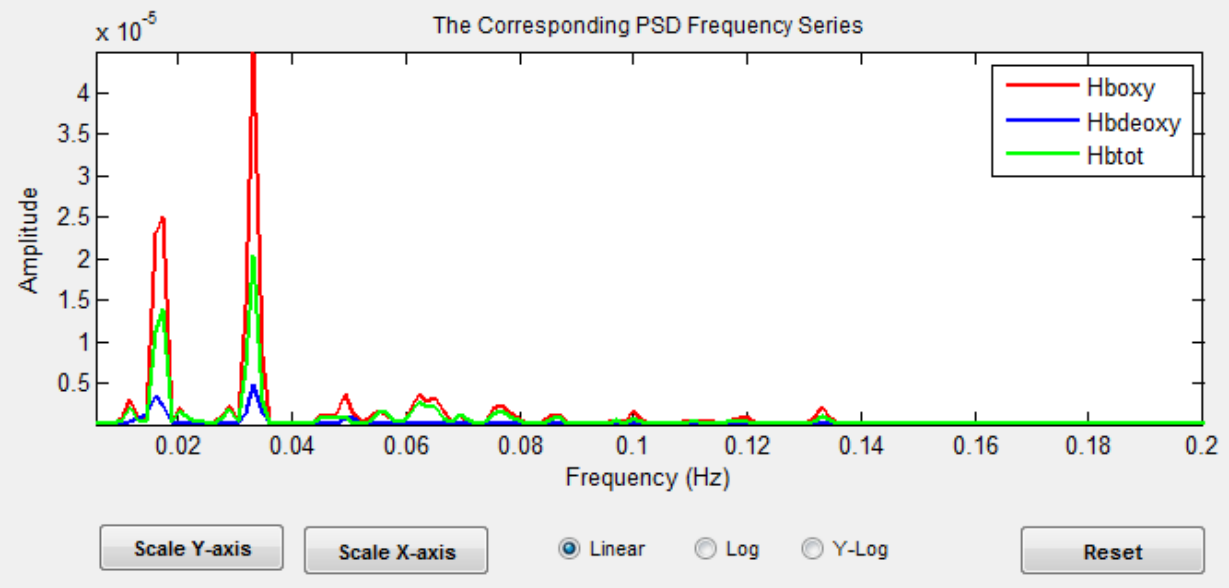


Figure 5-17. Detail view of the PSD plot window and associated user-control features in the *Time Series Data Viewer* GUI (Figure 5-3).

2.4.1 Rescale amplitude

You can rescale the vertical axes, by using the **Scale Y-Axis** buttons. By default, each data channel's PSD is scaled to its own minimum and maximum values. In contrast, using the **Scale Y-Axis** button will apply a user-defined scale range to all the channel-based PSD. The following is an example of use of the scaling function for rescaling the amplitude.

***Step 1*:** Click the **Scale Y-Axis** button to open a text field window as shown in Figure 5-18:

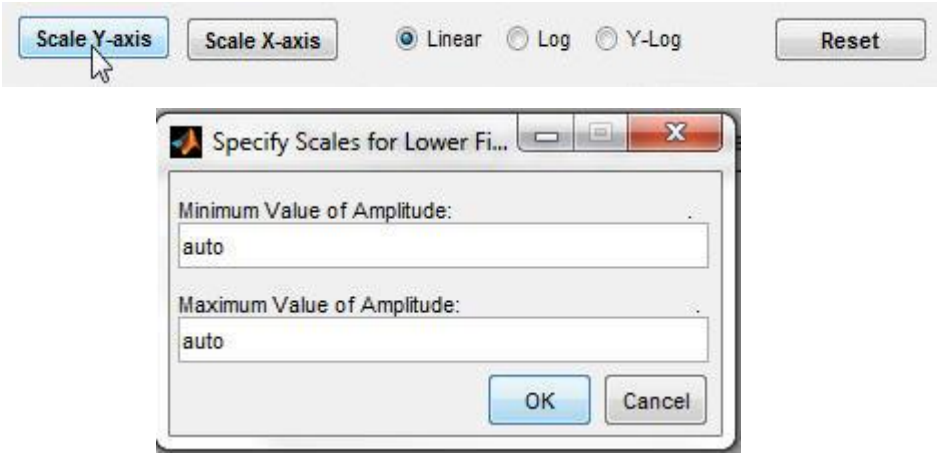


Figure 5-18. Rescaling the PSD amplitude.

***Step 2*:** Enter the desired minimum and maximum values for the display range of the vertical axis. An example of entered values are shown in Figure 5-19.

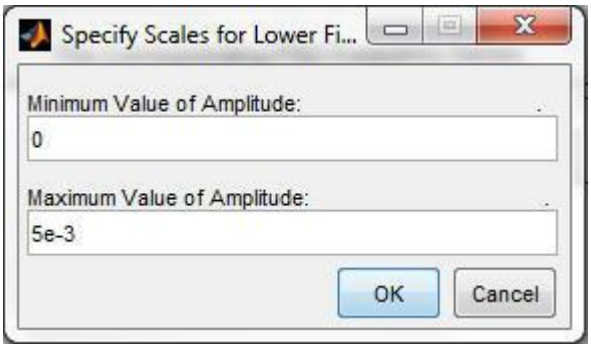


Figure 5-19. An example of rescaling the PSD amplitude.

***Step 3*:** Click the **OK** button to close the text field window. Illustrated in Figure 5-20 is an updated plot, with the new vertical scale limits (for this and the subsequent examples in Section 2.4, we intentionally work with PSDs derived from raw-data time series, so that the full frequency content present in fNIRS signals can be appreciated):

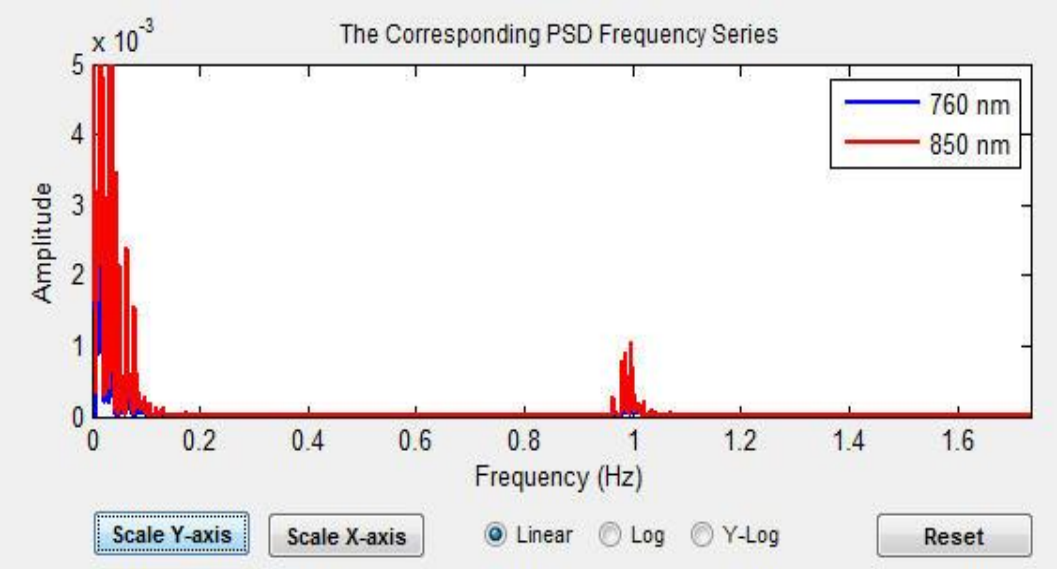


Figure 5-20. An example of displaying the rescaled PSD.

***Note*:** You can reset the minimum and maximum values of the vertical-scale range to their default values by typing "auto" in the corresponding text fields, as shown in Figure 5-21.

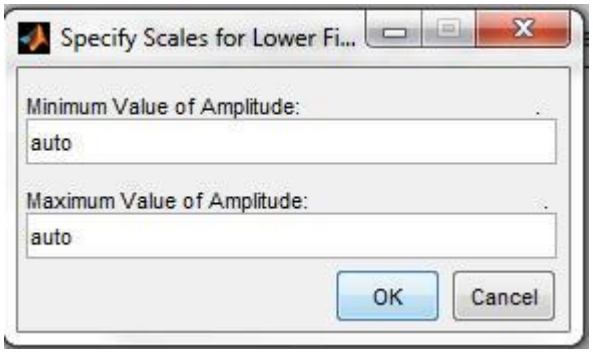


Figure 5-21. Reset the PSD scaling into default values.

2.4.2 Change Axes Scaling

There are three radio buttons: **Linear**, **Log** and **Y-Log** below the plot. Using them, you can plot data with linear or logarithmic scale. The following is an example of plotting data with different scales by use of these radio buttons.

As shown in Figure 5-22, when you click on the **Linear** radio button (this is the default case), the specified data sets are plotted with linear scale for both x- and y-axis.

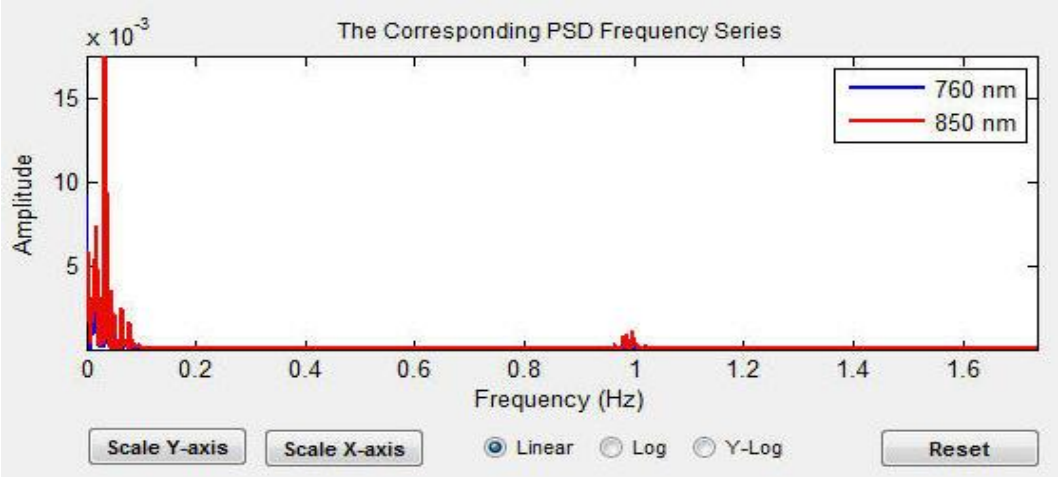


Figure 5-22. Plot PSD in linear scaling.

When you click on the **Log** radio button, the specified data sets are plotted with logarithmic scale for both x- and y-axis as seen in Figure 5-23.

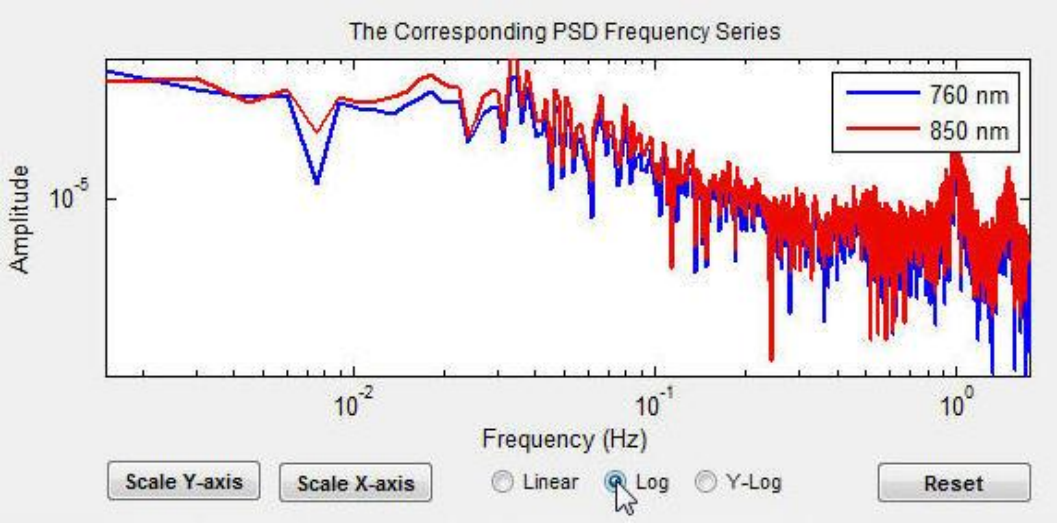


Figure 5-23. Plot PSD in logarithmic scaling.

When you click on the **Y-Log** radio button, the specified data sets are plotted with logarithmic scale for y-axis and linear scale for x-axis (see Figure 5-24).

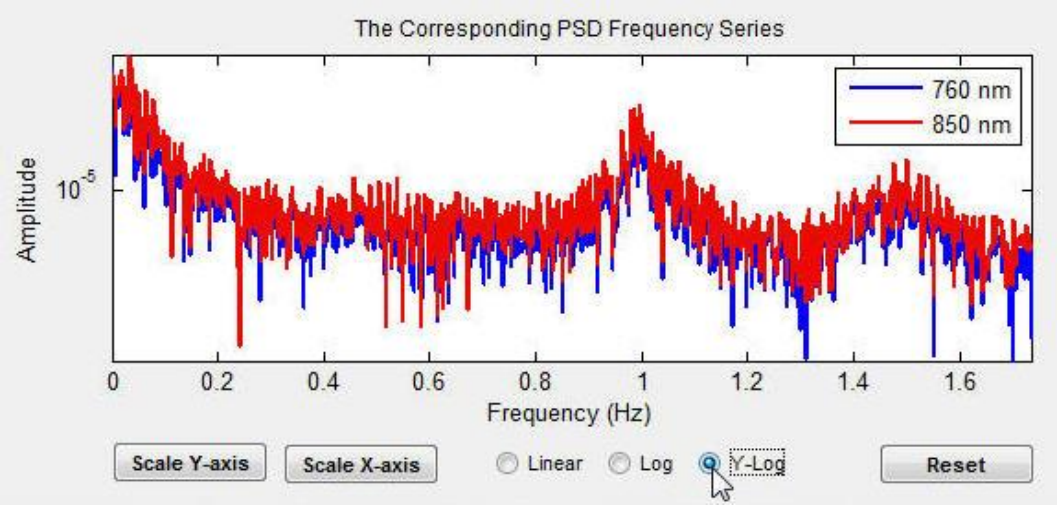


Figure 5-24. Plot PSD in semi-logarithmic scaling.

2.4.3 Change Frequency Interval

Clicking on the **Scale X-axis** button, you can graphically specify a frequency interval. This will enable a set of crosshairs, as illustrated in the Figure 5-25, that you can move by using the mouse. A frequency segment is indicated by twice clicking the primary mouse button, the first time to indicate the beginning of the frequency interval, and the second time to indicate the end of the frequency interval.

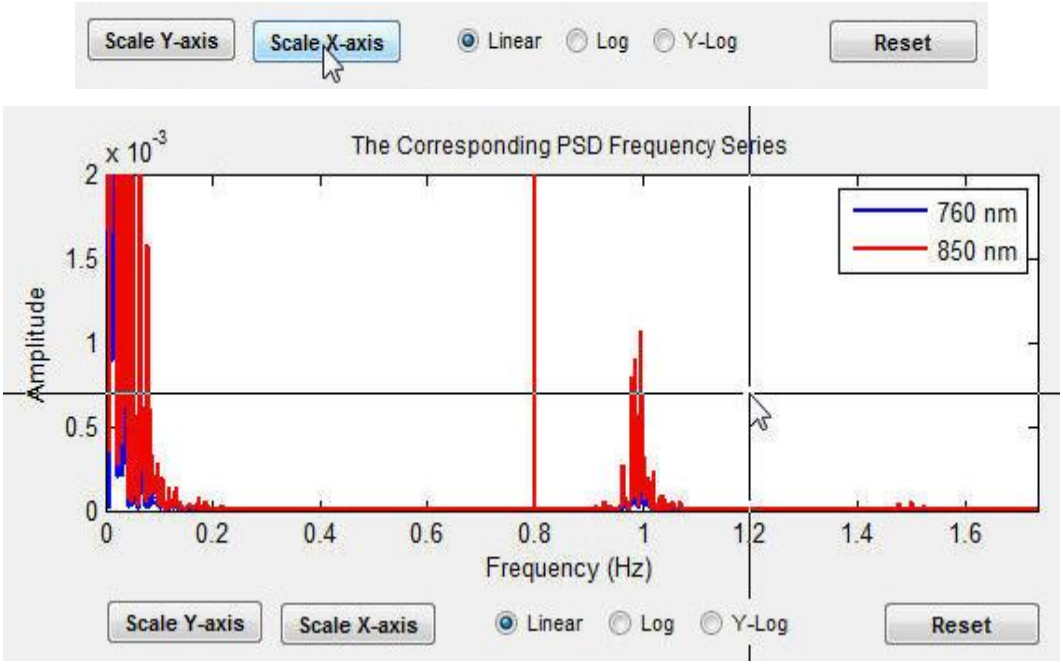


Figure 5-25. Change the plot frequency interval by moving mouse.

An updated plot of the PSD is produced, as shown in the Figure 5-26.

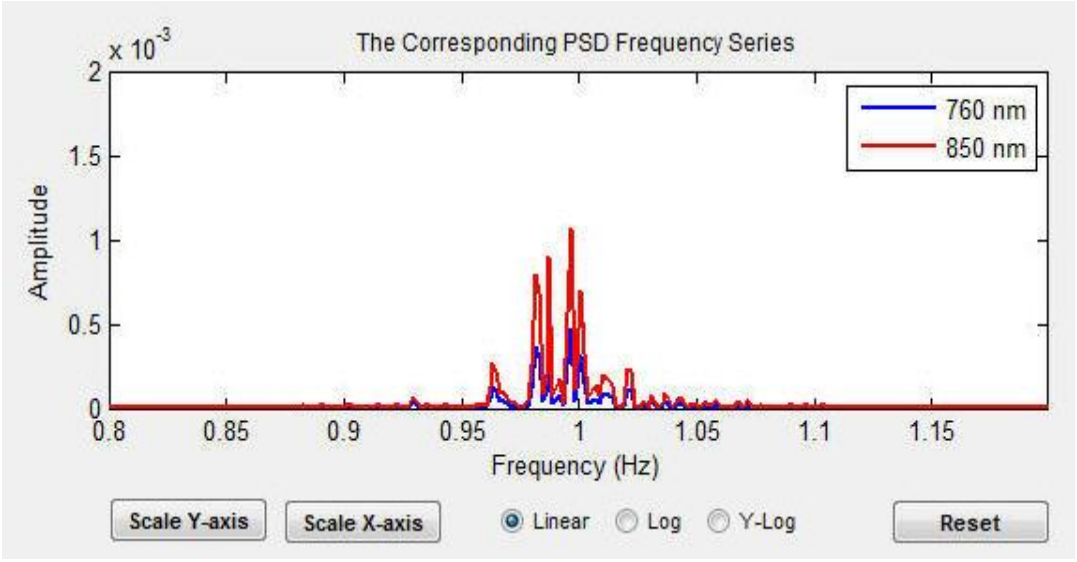


Figure 5-26. The PSD plot in changed frequency interval.

2.4.4 Resetting the Display Ranges

Press the **Reset** button in order to restore the starting and ending frequency values to their default values, as shown in the Figure 5-27:

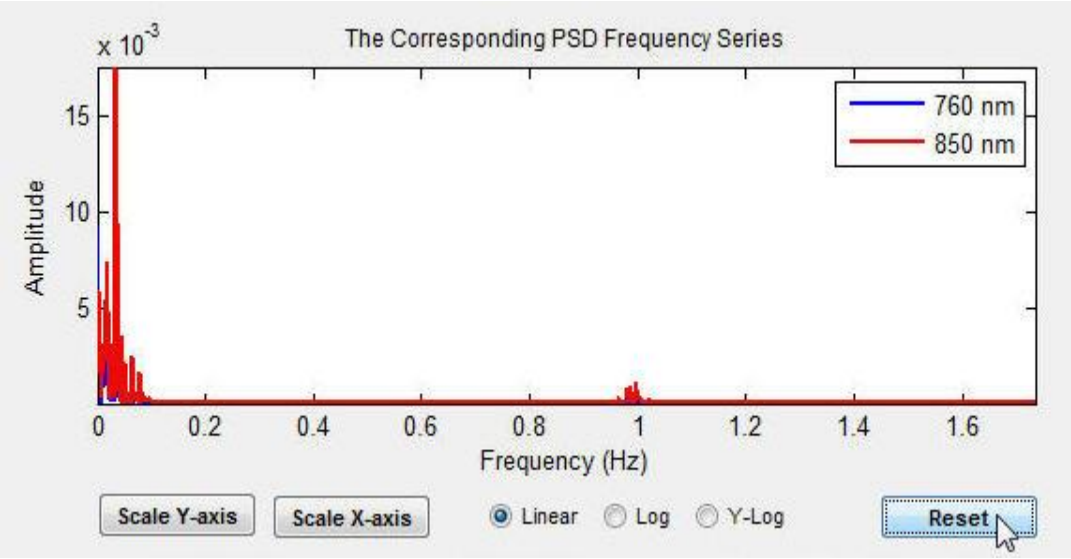


Figure 5-27. Reset the frequency interval to the default interval.

2.5 Saving a selected time series

The components in lower left highlighted corner of the Data Viewer GUI, as shown in Figure 5-28, allow you to save one or more specific time series, displayed in either the upper or lower sub-figures, into ASCII files with user-defined filenames. This functionality can be useful if you discover an interesting temporal behavior that you want to use subsequently in additional processing steps.

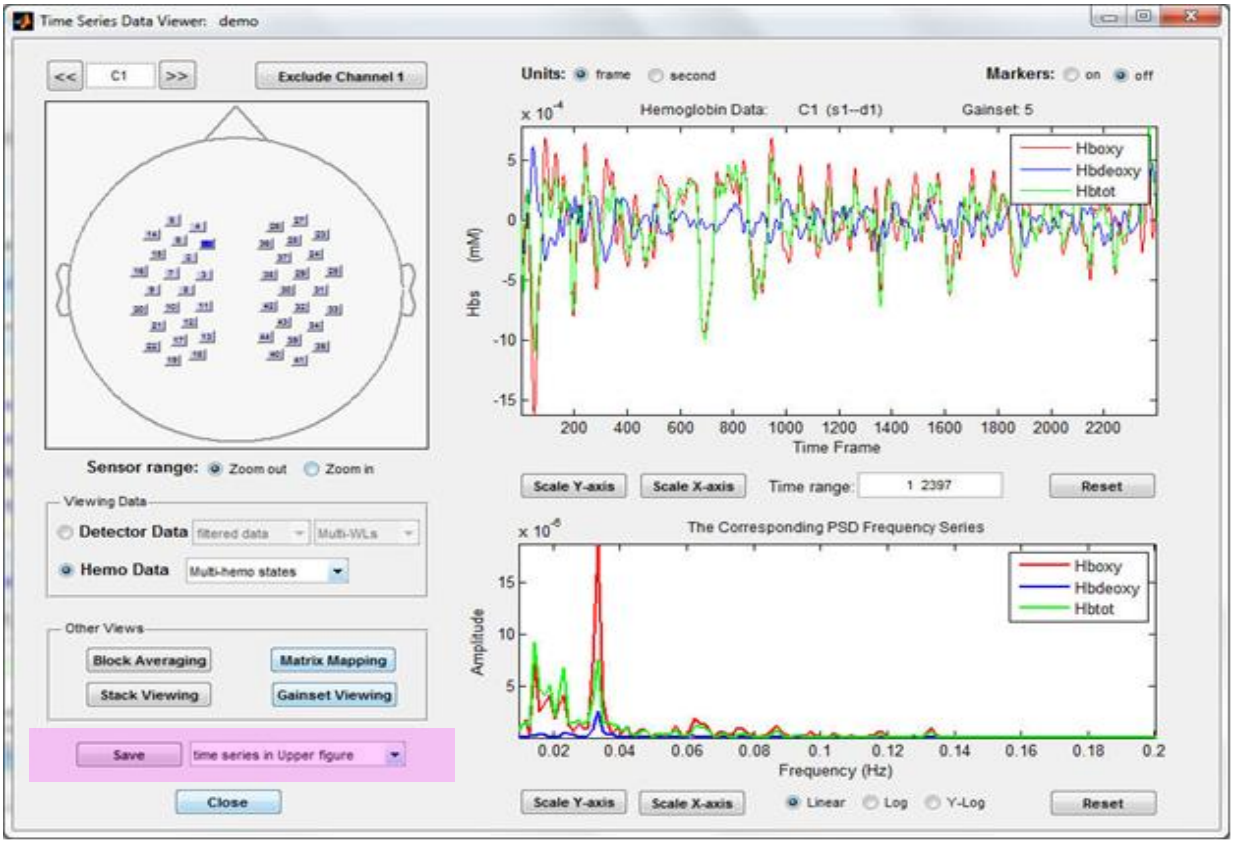


Figure 5-28. Saving data components in the *Time Series Data Viewer* GUI (highlighted).

The following is an example of saving a selected time series.

***Step 1*:** Click the pull-down menu to select a time series to be saved, as shown in Figure 5-29:

Figure 5-29. Menu for selecting a time series or SD to be saved (enlarged view of the GUI component that is highlighted in Figure 5-28).

***Step 2*:** Click the **Save** button to open a browser window for saving the data, as shown in Figure 5-30:

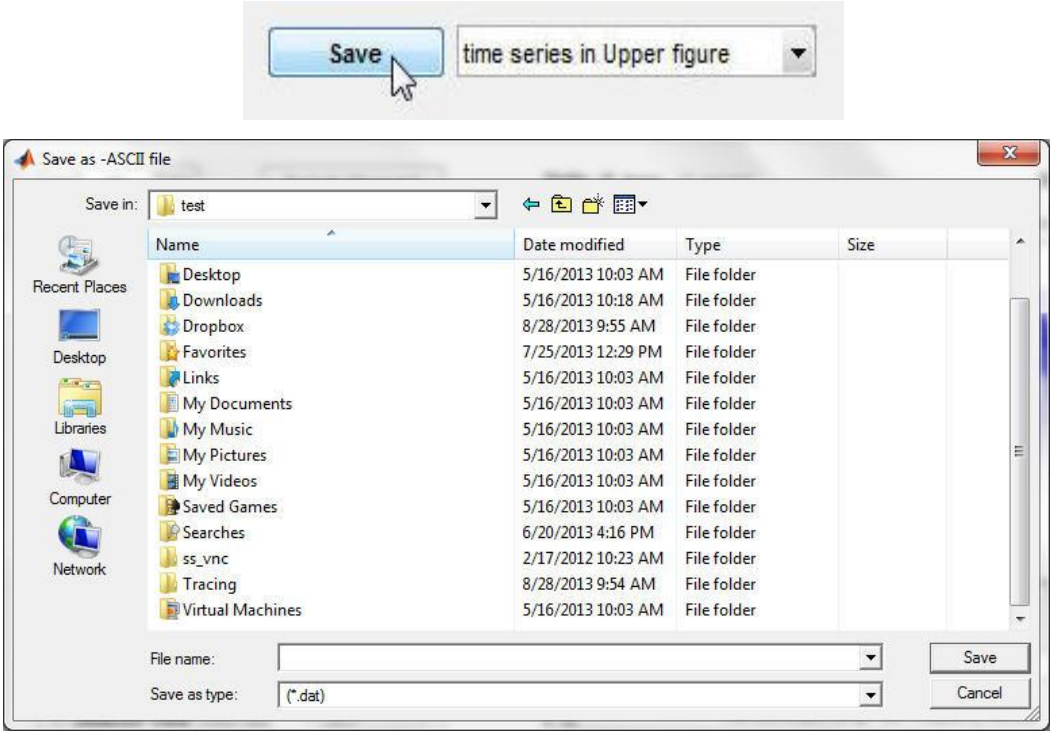


Figure 5-30. Select a desired folder and a file name to save the data.

Step 3: Use the browser window to navigate to the folder where your selected data will be saved in, type a desired file name in the **File name** field, then click the browser window **Save** button to store your data.

2.6 Viewing time series data in different formats

As shown in Figure 5-31, the components in lower left corner (highlighted field) of the Data Viewer GUI allow you to view a specified time series data set in a number of different display formats. These components consist of four push buttons:

Block Averaging button: for viewing the block average time series data sets;

Matrix Mapping button: for mapping all the time series data sets;

Stack Viewing buttons: for viewing the time series data in stacked format;

Gainset Viewing button: for mapping the all channel gain settings.

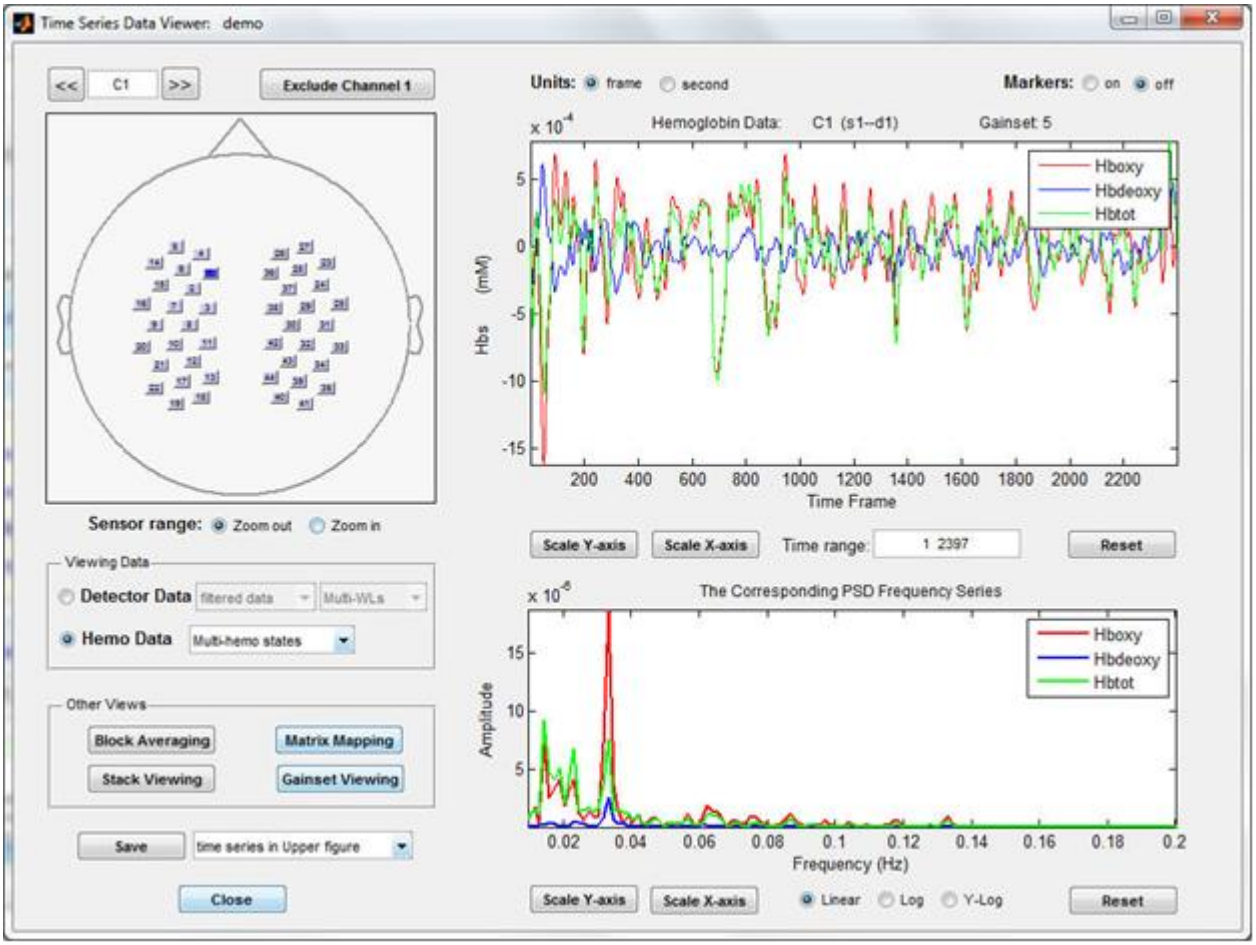


Figure 5-31. Other viewing components in the *Time Series Data Viewer* GUI (highlighted).

The following subsections will show you how to use these functions to view time series data sets in a different format.

2.6.1 Stack viewing

This choice (*i.e.*, stack viewing) allows you to display a selected number of detector-data time series simultaneously in a stacked format, over any desired interval of time frames. Several controls are provided to allow adjustment of the number of time series displayed and the vertical and horizontal axis scales. The following is an example of application of the **Stack Viewing** function. Clicking the **Stack Viewing** button will bring up a new GUI, as shown in Figure 5-32. Using the GUI, you can view the time series data sets you have selected in the stacked format.

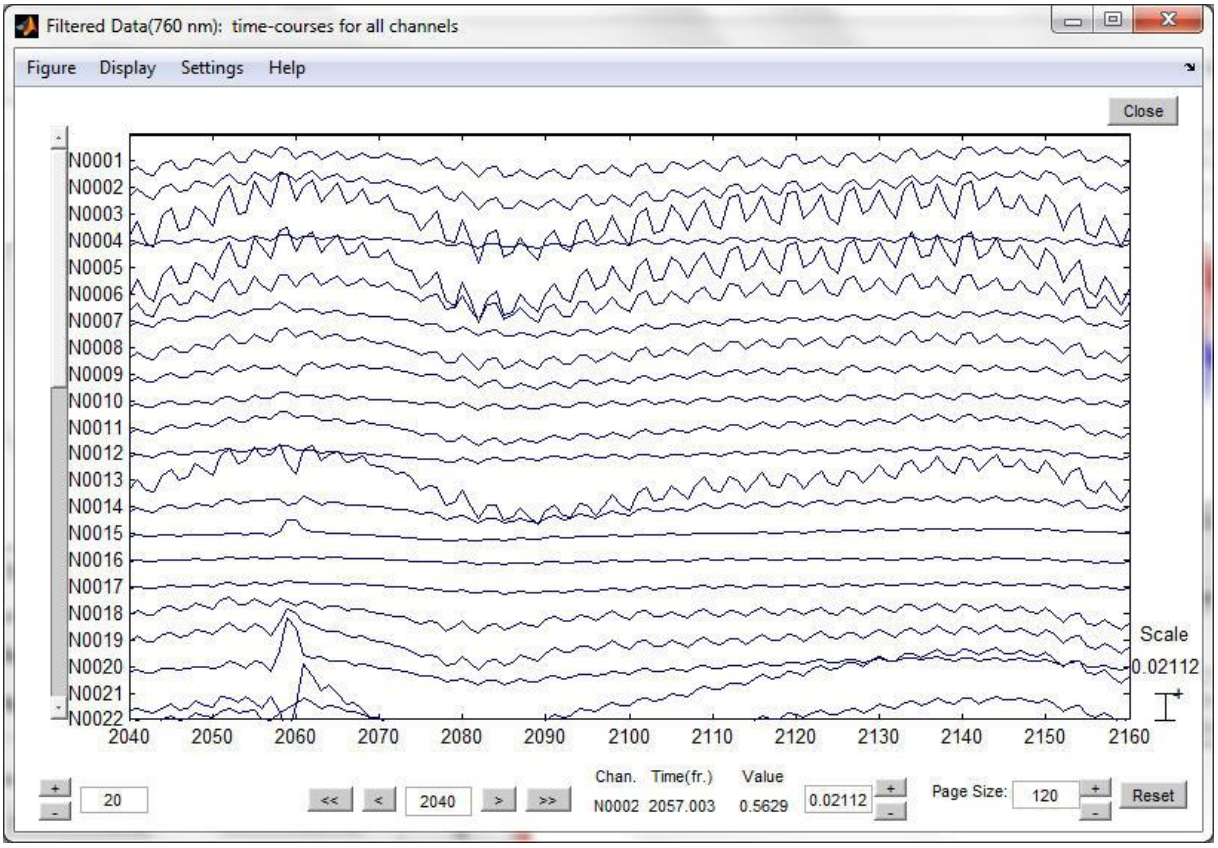


Figure 5-32. Viewing time series data sets in stacked format.

2.6.2 Matrix mapping

This choice (*i.e.*, Matrix Mapping) allows you to display the specified data set as a contour surface, with time plotted along the x-axis and source-detector/nirs channel along the y-axis. An example of application of the **Matrix Mapping** function is shown in Figure 5-33. Clicking the **Matrix Mapping** button will bring up a new GUI named Time Series Data Mapping. In the new GUI you can change the color scale of the map by using the **Scale C-bar** button, change time interval by using the **Scale X-axis** button or the **Time Range** field, and select desired channel interval by using the **Scale Y-axis** button or the **Channel Range** field. You can also export the mapping figure or the mapping data by using the **Save** button.

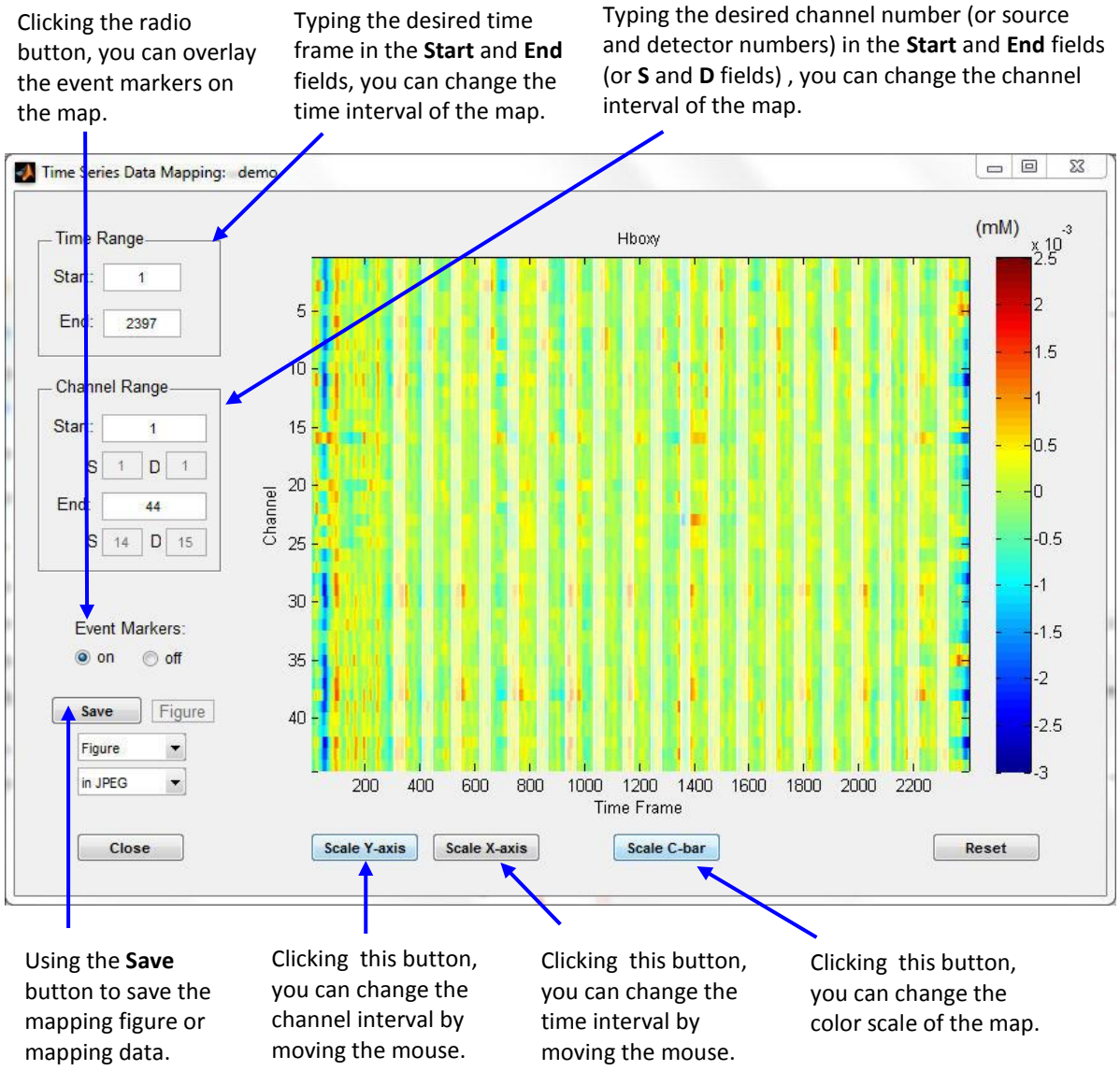

Clicking the radio button, you can overlay the event markers on the map.
Typing the desired time frame in the Start and End fields, you can change the time interval of the map.
Typing the desired channel number (or source and detector numbers) in the Start and End fields (or S and D fields) , you can change the channel interval of the map.
Time Series Data Mapping: demo
Time Range
Start: 1
End: 2397
Channel Range
Start: 1
S 1 D 1
End: 44
S 14 D 15
Event Markers:
on
off
Save
Figure
Figure
in JPEG
Close
Hboxy
(mM)
x 10^-3
Channel
Time Frame
Scale Y-axis
Scale X-axis
Scale C-bar
Reset
Using the Save button to save the mapping figure or mapping data.
Clicking this button, you can change the channel interval by moving the mouse.
Clicking this button, you can change the time interval by moving the mouse.
Clicking this button, you can change the color scale of the map.

Figure 5-33. Viewing time series data sets in matrix mapping format.

2.6.3 Block Averaging

This choice allows you to block-average the specified time series data sets over the block segments defined in the event file that you have created, and to display the block-averaged time series of all nirs channels on their own channel positions of head surface that you have specified in your probe setup. An example of application of the **Block Averaging** function is shown in Figure 5-34. Clicking the **Block Averaging** button will bring up a new GUI named Block Averaging.

Using the **Hemo Data** radio buttons and the followed pull-down menus, you can select your desired time series data set for block averaging.

Using these **Time units** radio buttons, you can change the time unit in the block averaging plot.

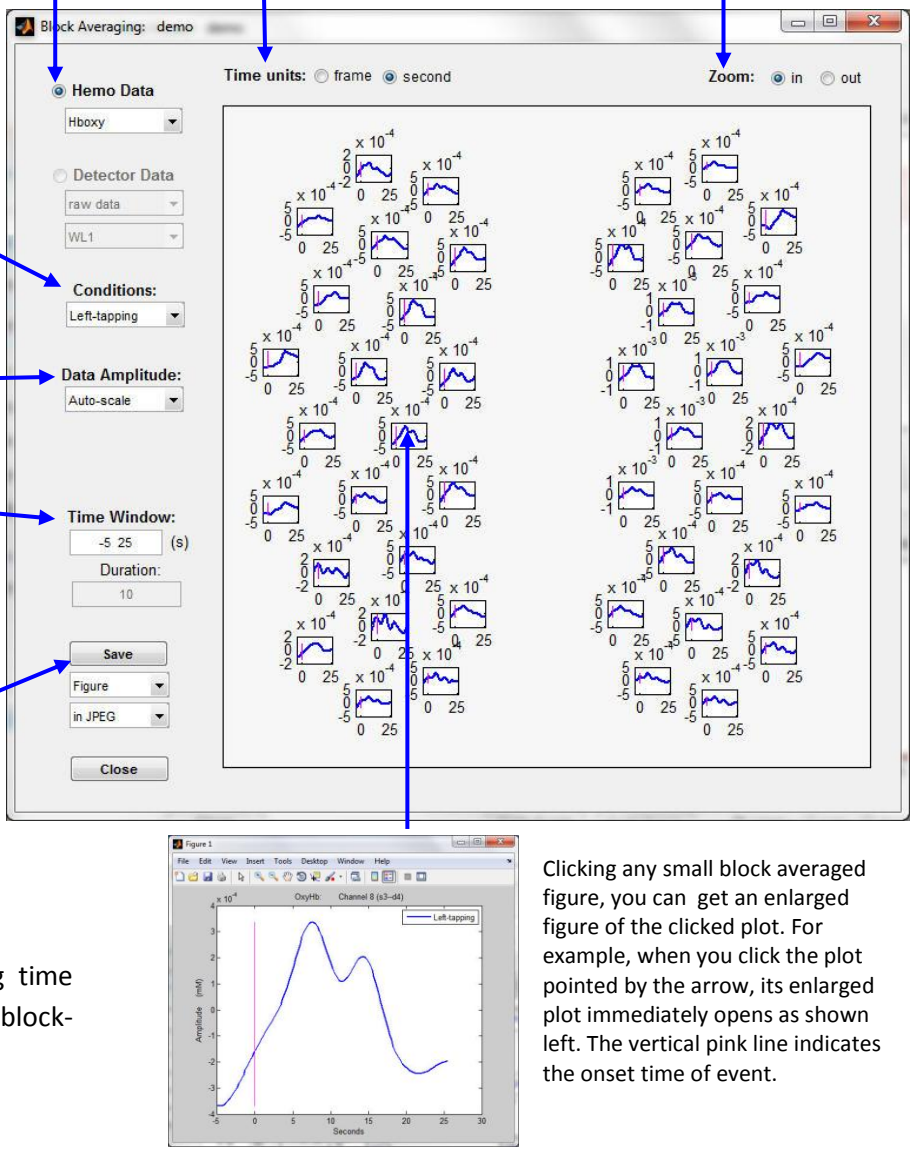
Using these **Zoom in/out** radio buttons, you can map the block averaging plot on head surface.

Using the **Condition** pull-down menus, you can select your desired condition data set for block averaging.

Using the **Data Amplitude** pull-down menus, you can select your desired data amplitude scale for block averaging plot.

Using the **Time Window** text field , you can set the block average time interval. Negetive value means the time before event onset.

Using the **Save** button, you can save the block averaging figure or block averaged time series data.



Clicking any small block averaged figure, you can get an enlarged figure of the clicked plot. For example, when you click the plot pointed by the arrow, its enlarged plot immediately opens as shown left. The vertical pink line indicates the onset time of event.

Figure 5-34. Viewing time series data sets in block-averaged format.

2.6.4 *Gainset Viewing*

Sometimes you may want to check the quality of your raw data sets by using the experimental gain settings. This choice (i.e., Gainset Viewing) allows you to display the experimental gain settings as a contour surface, with detector index along the x-axis and source index along the y-axis. An example of application of the **Gainset Viewing** function is shown here. Clicking the **Gainset Viewing** button will bring up a gain setting map as shown in Figure 5-35.

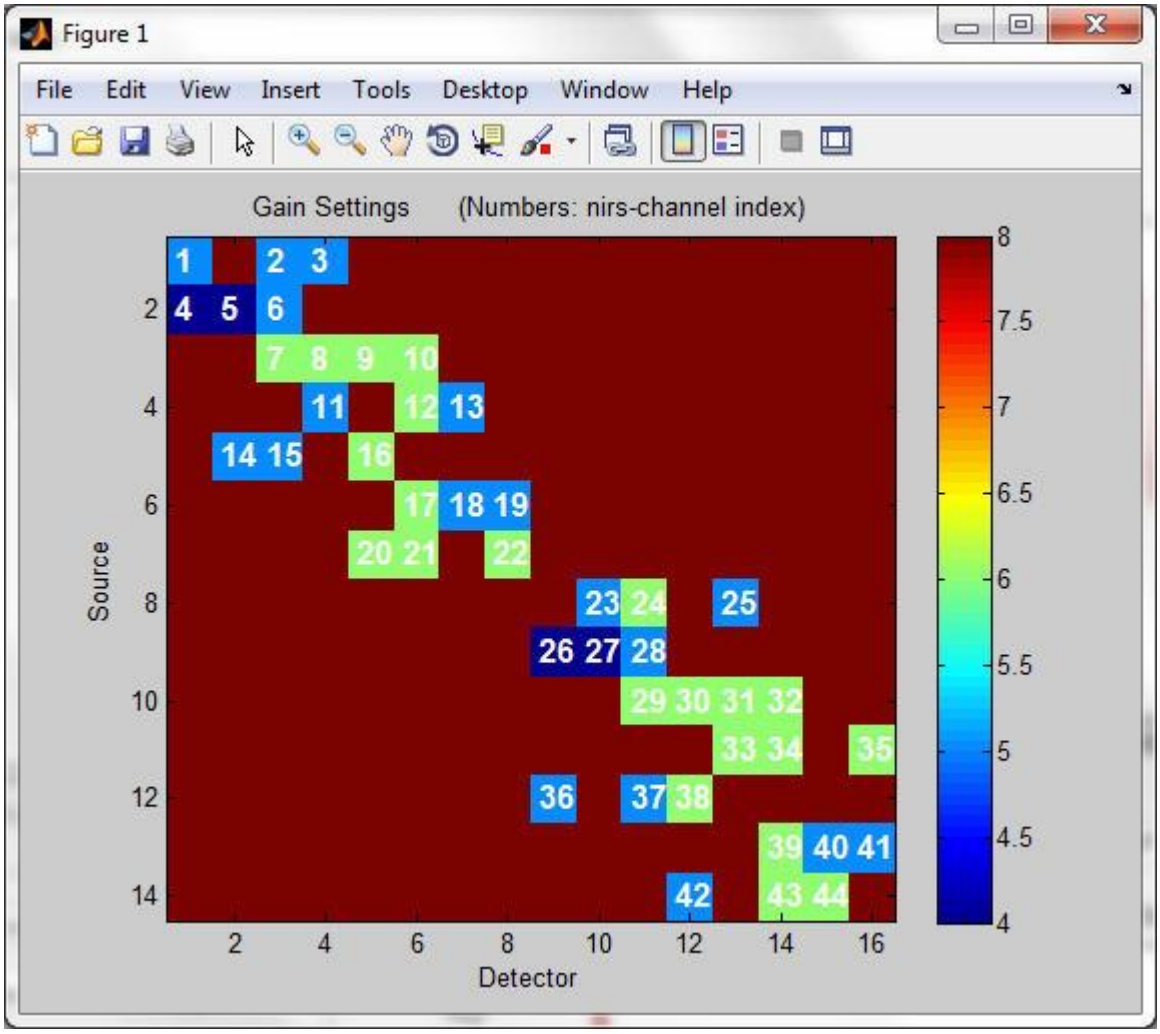


Figure 5-35. Viewing the gain settings of the raw data sets.

3 Map Hemodynamic States: all states

Pressing the **Map** Hemodynamic States button opens a progress bar to show the process of initializing the mapping data, then, a few seconds later, will bring up a new GUI named Topographic Mapping, as shown in Figure 5-36, which allows you to topographically map all hemoglobin images onto head and brain surfaces.

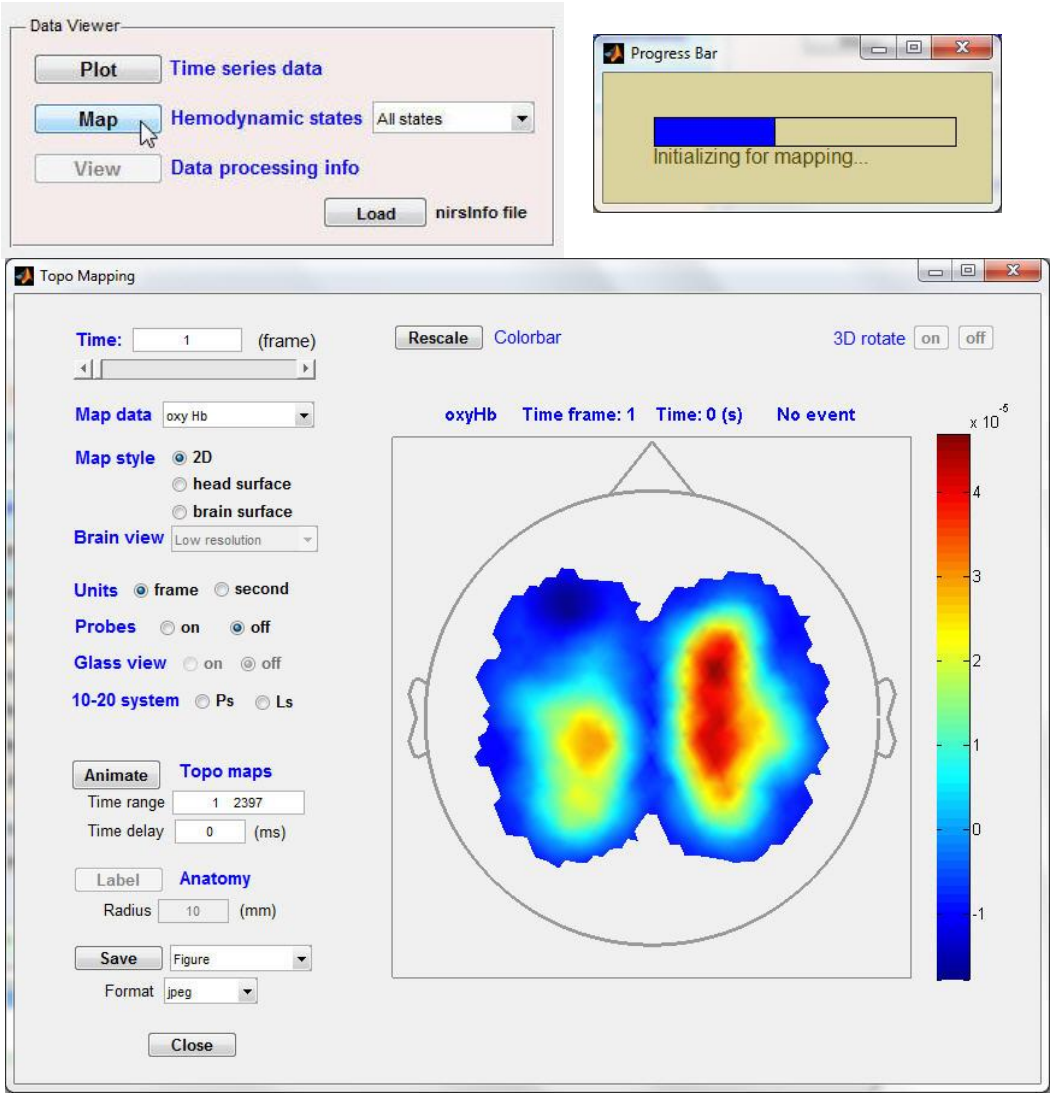


Figure 5-36. Mapping all hemodynamic states and the Topographic Mapping GUI**.**

The functionalities provided by the module are:

- Topographically map hemoglobin images onto head and cortex surfaces.
- Animate the hemoglobin time series maps for specified time interval.
- Label the brain anatomy in specified position on cortex surface (under development).
- Export the mapping figures and movies.

In addition, the module offers control functions that allow you to easily:

- Switch to a different mapping variable (*e.g.*, from oxy-Hb concentration to deoxy-Hb concentration, to total-Hb concentration, and to HbO_2 saturation);

- Switch to a different topographic mapping styles (e.g., from 2D to head surface, and to brain surface);
- Select which specific time frame/second to map and time interval to animate;
- Change color scales of the map and movie.

3.1 Selecting specific time frame/second for mapping

The components in upper left corner of the Topographic Mapping GUI allow you to select a specific time frame/second hemoglobin data to map. These components consist of a text field and slider, as shown in Figure 5-37.

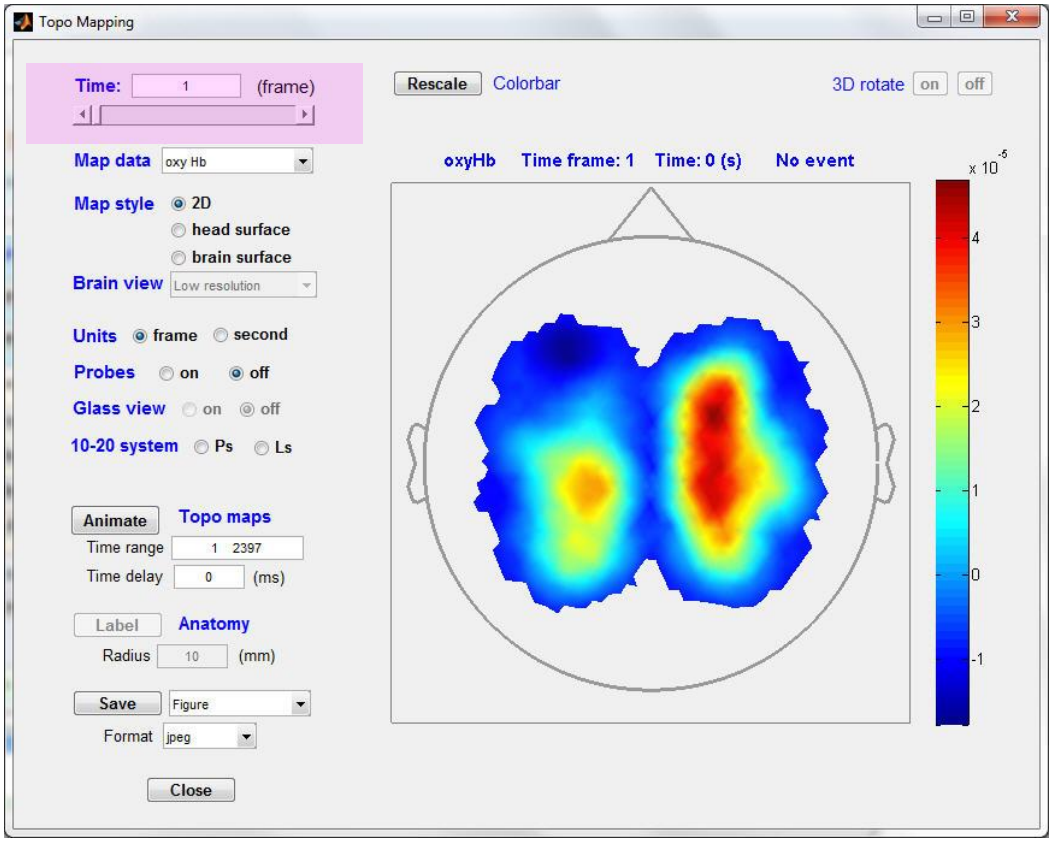


Figure 5-37. Selecting specific time frame/second for mapping**.**

There are two ways to select a specific time frame/second data set to map. One is to directly type your desired time frame/second in the **Time** text field, the other is to click slider to scroll it to your desired time frame/second. When you type a new time frame/second value in the text field and then click the Enter key or left mouse key, the position of the slider and the hemoglobin map will update automatically. Similarly, when you scroll the slider, the value in the text field and the hemoglobin map will also update almost at the same time.

An example of selecting a hemoglobin data set at a specific time to map shows here. When the time frame 120 is selected by typing it in text field or scrolling the slider, you can see the updated hemoglobin map as shown in Figure 5-38.

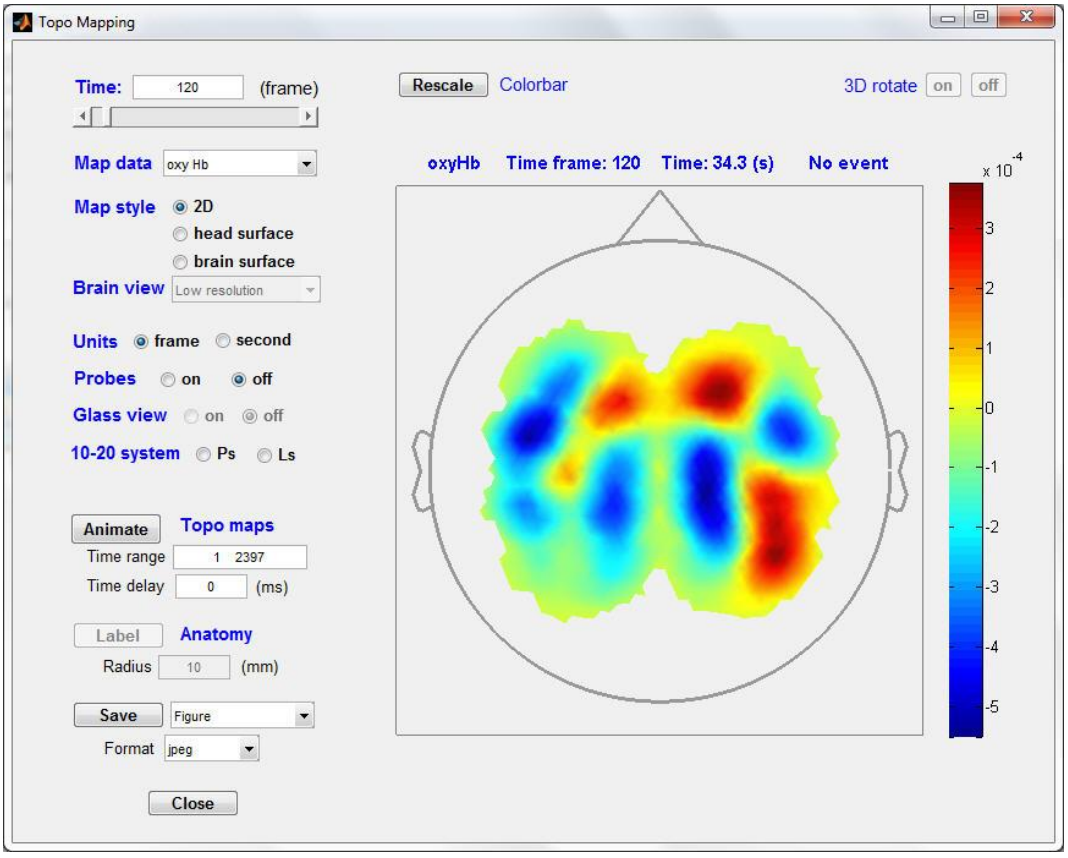


Figure 5-38. An example of selecting a specified time frame state for mapping**.**

3.2 Selecting specific hemoglobin data set to map

The **Map data** pull-down menu in the upper left side of the Topographic Mapping GUI, as shown in highlighted in Figure 5-39, allow you to select a specific hemoglobin data set for mapping.

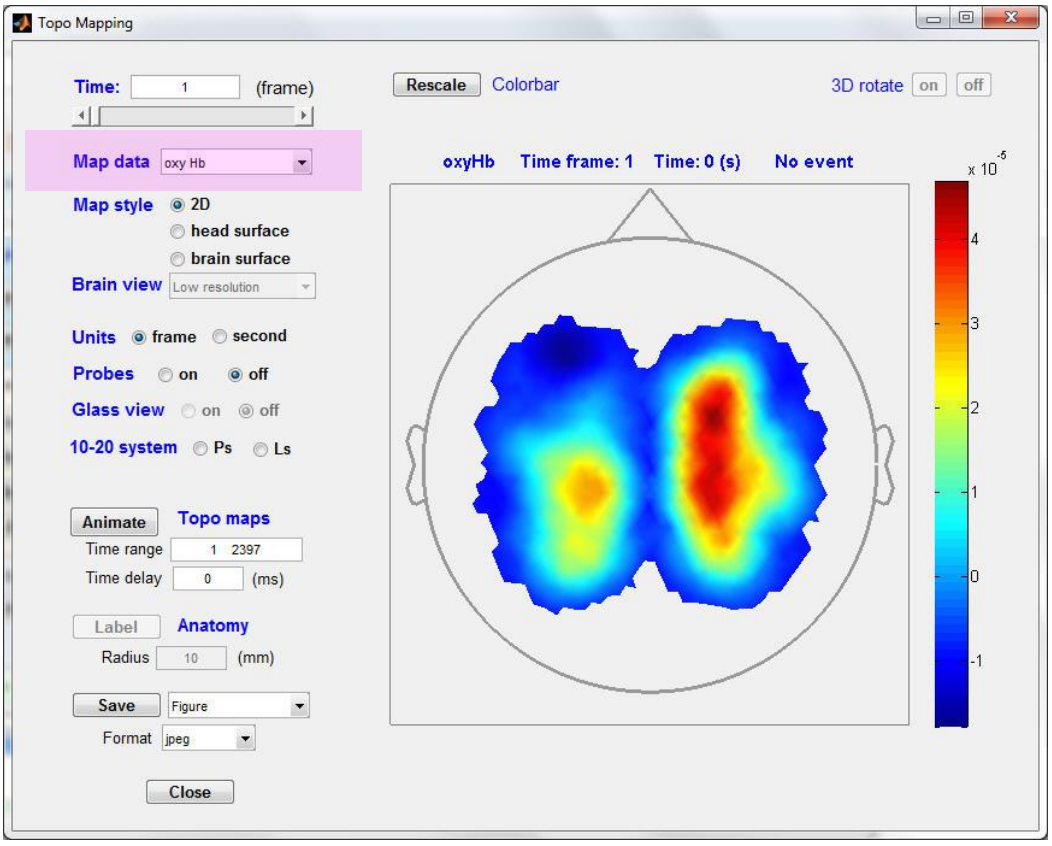


Figure 5-39. Selecting specific hemoglobin data set to map.

As shown in Figure 5-40, when you click the **Map data** pull-down menu, you can see that four kinds of hemoglobin data set are listed in the menu: oxy Hb (this is the default case), deoxy Hb, and total Hb. As you choose one of the data sets in the list, the topographic map will immediately update to what you selected hemoglobin data set.

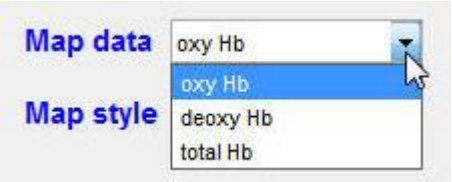


Figure 5-40. The Map data pull-down menu for specifying hemodynamic data set to map.

3.3 Selecting different topographic mapping styles

The components in the upper left side of the Topographic Mapping GUI, as shown in highlighted in Figure 5-41, allow you to select different topographic maps for viewing. The components consist of:

Three **Map style** radio buttons: for different topographic mappings;

Brain view pull-down menu: for different cortex mappings.

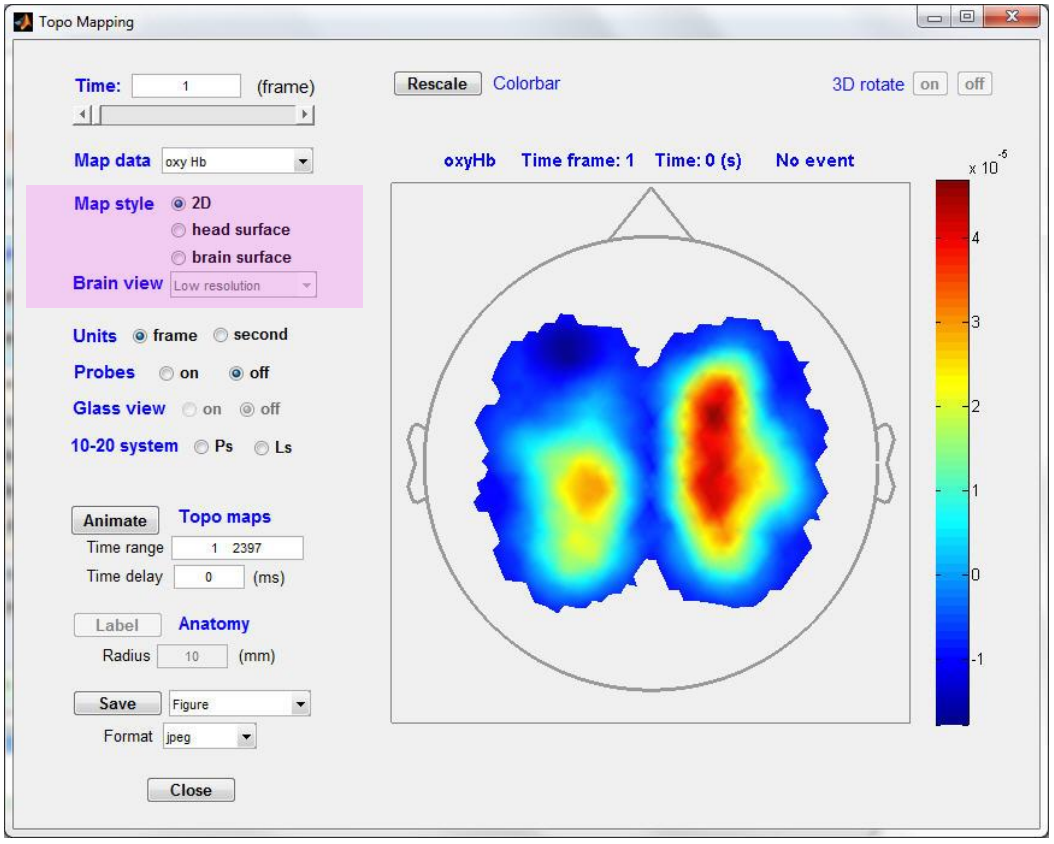


Figure 5-41. Selecting different topographic mapping styles**.**

By default, the **2D** radio button have been selected and the specified hemoglobin data set is mapped onto the 2D head surface, as shown above. When you click the **head surface** radio button, the specified hemoglobin data set will be mapped onto (3D) head surface, and the brain surface radio button onto (3D) cortex surface. The following figures show examples of different topographic mappings.

When the **head surface** radio button is chosen, you can see the updated topographic map as shown in Figure 5-42.

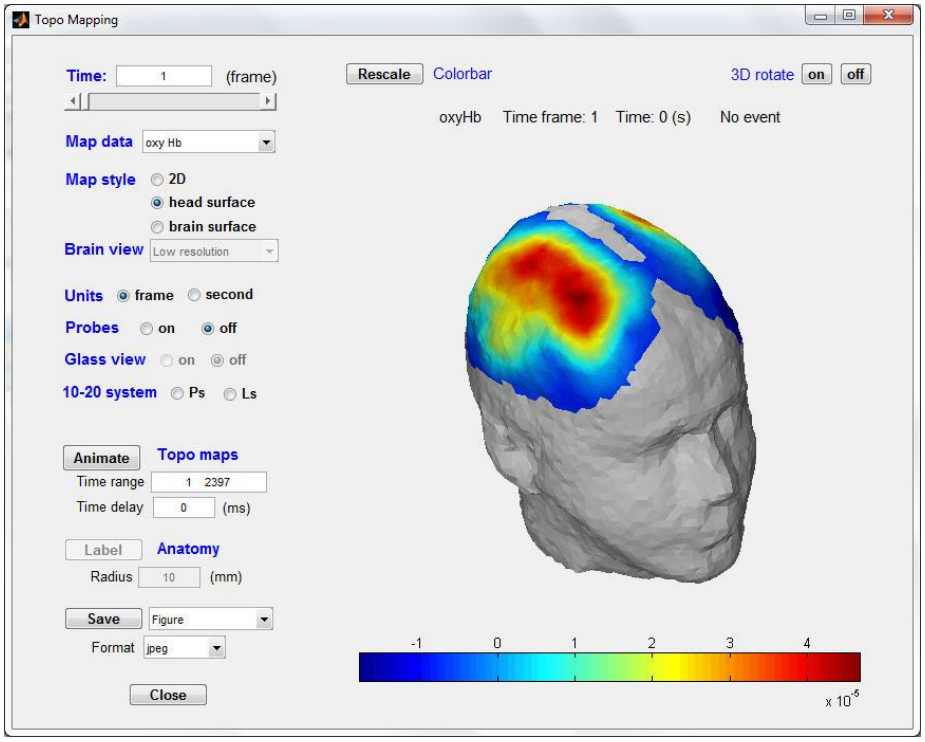


Figure 5-42. The data sets mapping onto (3D) head surface.

When the **brain surface** radio button is chosen, the updated topographic map is shown in Figure 5-43.

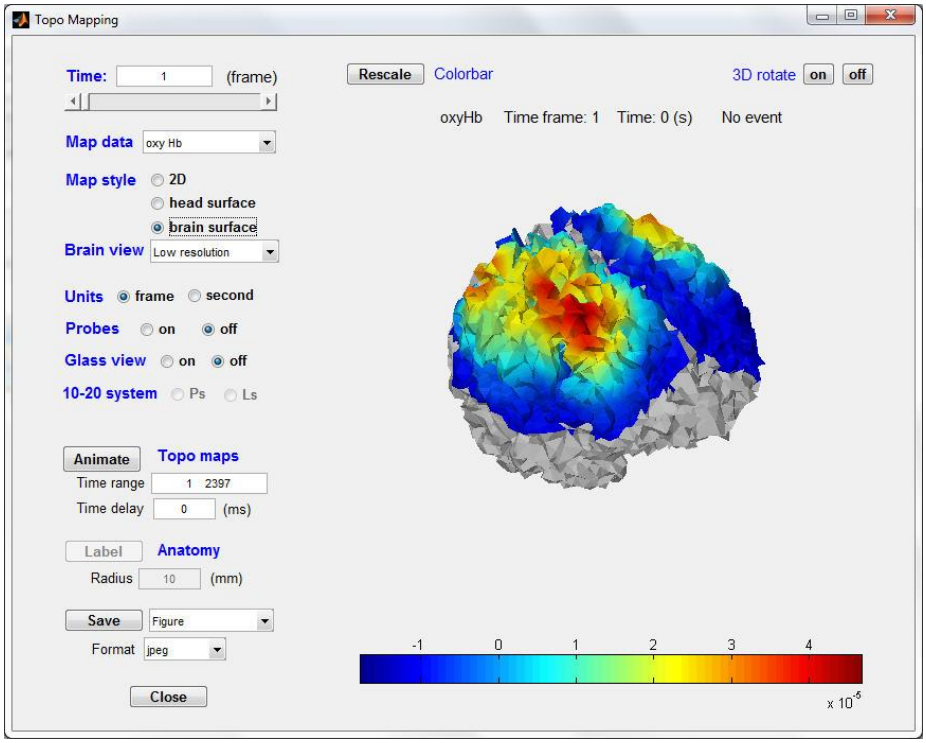


Figure 5-43. The data sets mapping onto (low resolution) brain surface.

As you have seen in the figure above, when you click the **brain surface** radio button, the **Brain view** pull-down menu below the radio button enables. If you click the pull-down menu, you can see that there are three options listed in the menu: Low resolution, High resolution and High resolution MNI, as shown in Figure 5-44. The default case is the first option, the hemoglobin data is mapped onto a low resolution cortex surface.

Figure 5-44. The brain view pull-down menu for selecting different cortex mapping.

If you want to map the specified hemoglobin data set onto a high resolution brain surface or a MNI averaged brain surface, you can select the options: High resolution or High resolution MNI in the **Brain view** pull-down menu. Figures 5-45 and 5-46 show the topographic maps when the two options are selected, respectively.

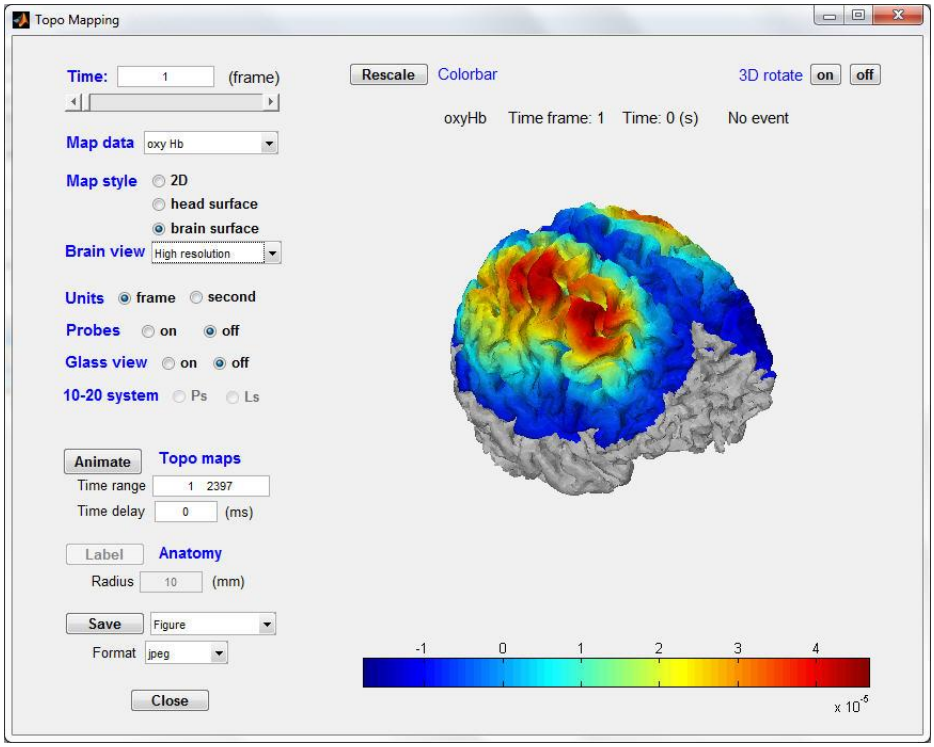


Figure 5-45. The data sets mapping onto (high resolution) brain surface.

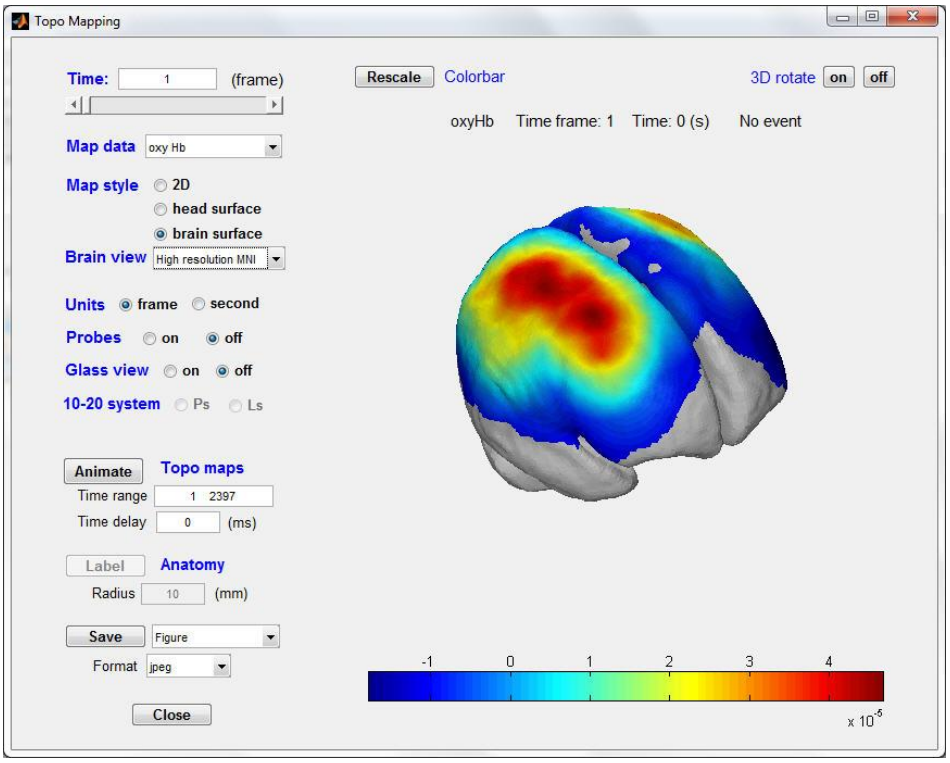


Figure 5-46. The data sets mapping onto MNI brain surface.

3.4 More controls on topographic mapping

The components in the middle left side of the Topographic Mapping GUI, as shown in highlighted in Figure 5-47, provides you with more controls to view the topographic maps. Using these controls, you can change time unit, plot the probes (sources and detectors) arrangement on the map, show the EEG extended 10-20 system points and labels on the head surface map, and view the topographic cortex map with a transparent head surface (Glass viewing). The controls consist of:

Two **Units** radio buttons: for changing time unit;

Two **Probes** radio buttons: for plotting the probes;

Two **Glass view** radio buttons: for glass viewing the cortex map;

Two **10-20 system** radio buttons: for showing 10-20 system points on the map.

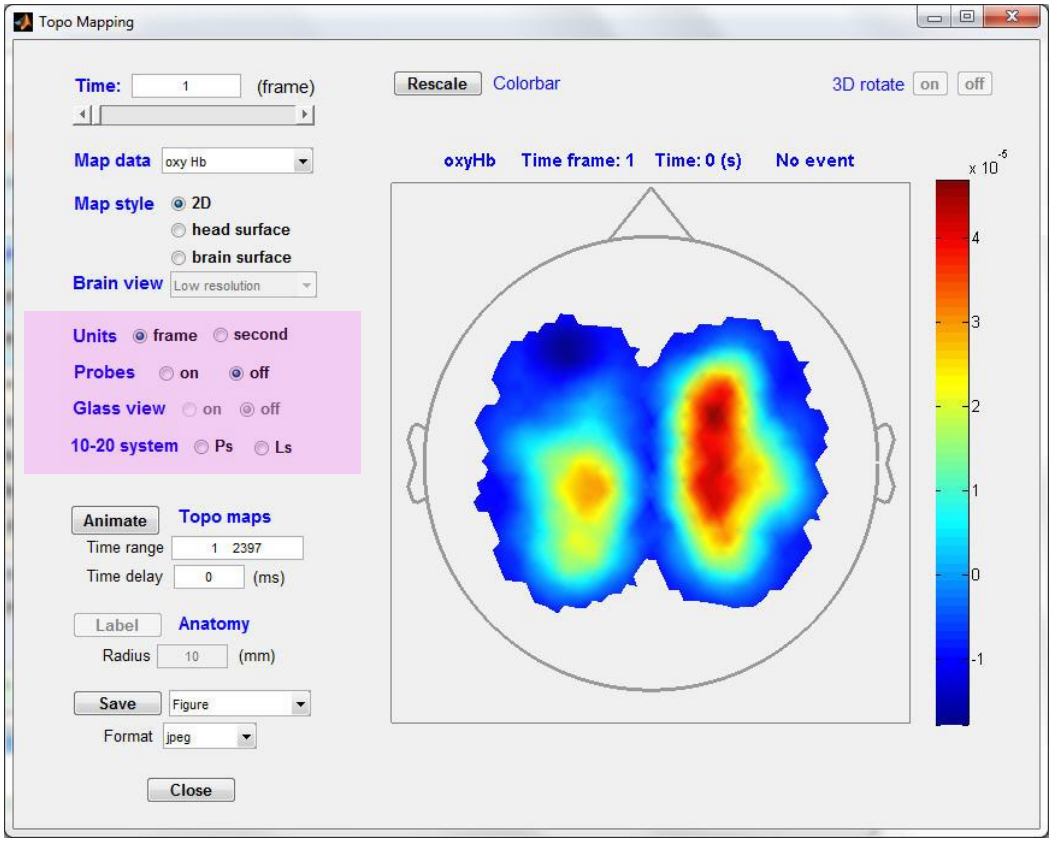


Figure 5-47. More controls on topographic mapping.

3.4.1 Changing time unit

Using the **Units** radio buttons: **frame** and **second**, you can switch the time unit between time frame and second by clicking these two buttons. By default, the time unit is frame, as shown in Figure 5-47. If you want to change the time unit to second, just click the **second** radio button, as shown in Figure 5-48. After the button is selected, the values in the **Time** text field (in top of the right figure) and the Time range text field (below the Animate button) are automatically converted in second. In this case, if you type values in these two fields, the values must be in seconds.

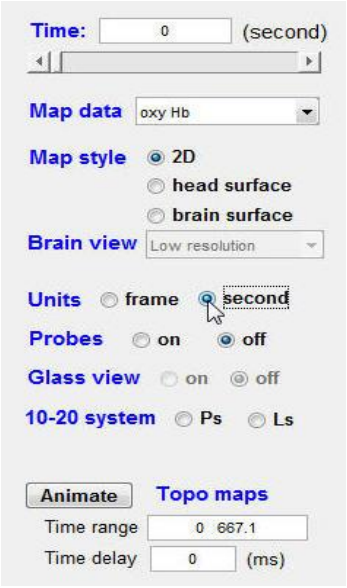


Figure 5-48. Changing the time unit.

3.4.2 Showing source/detector arrangement

Clicking the **Probes on** radio button, you can view the sources/detectors arrangement on the topographic map. If you don't want show the probes arrangement on the map, just click the **Probes off** radio button (this is the default case). Figures 5-49, 5-50 and 5-51 show the examples of plotting the probes arrangement on the 2D, head surface and brain surface topographic maps, respectively. In the figures, the red dots or small red balls are the sources and the yellow dots or small yellow balls the detectors.

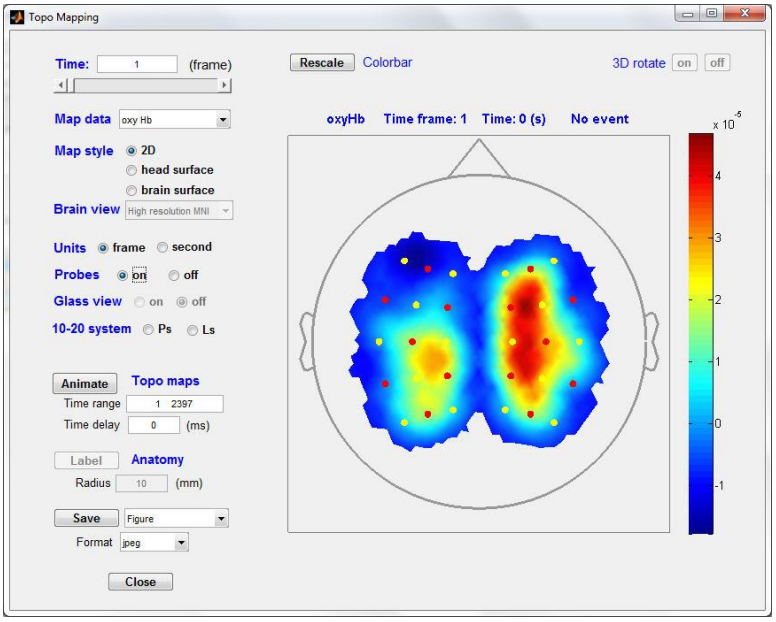


Figure 5-49. The probes arrangement mapped on the 2D head surface**.** The red dots are sources and yellow dots detectors.

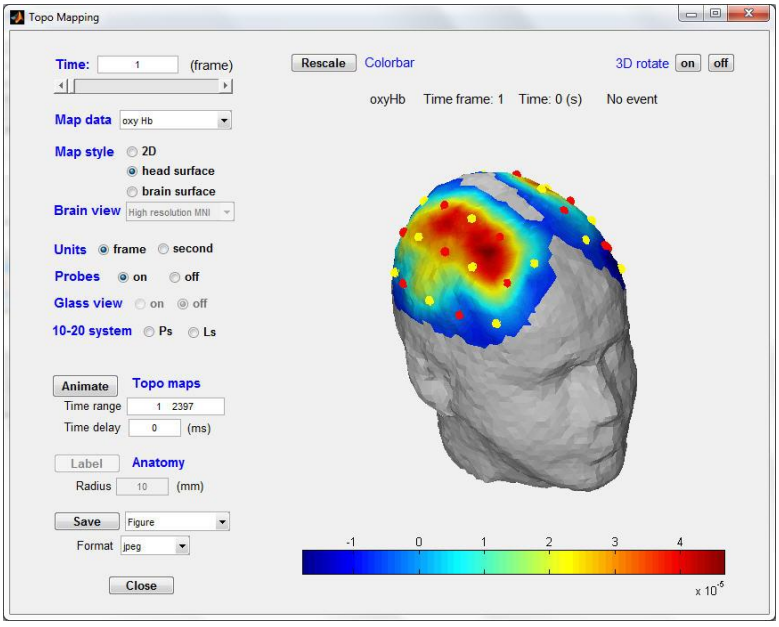


Figure 5-50. The probes arrangement mapped on the 3D head surface**.** The red dots are sources and yellow dots detectors.

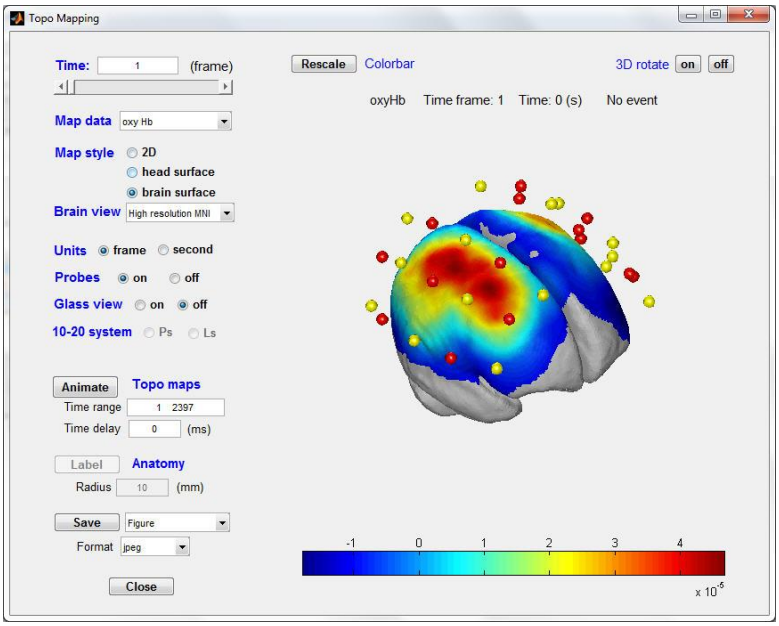


Figure 5-51. The probes arrangement mapped above the brain surface**.** The red balls are sources and yellow balls detectors.

3.4.3 Glass view Plotting

When you choose to map the specified hemoglobin data set onto cortex surface (*i.e.*, the **brain surface** radio button is selected), the two **Glass view** radio buttons: **on** and **off** are enabled. Clicking the **on** radio button next to the words **Glass view**, you can view the topographic cortex map with a transparent head surface. An example of glass-viewing is shown in Figure 5-52.

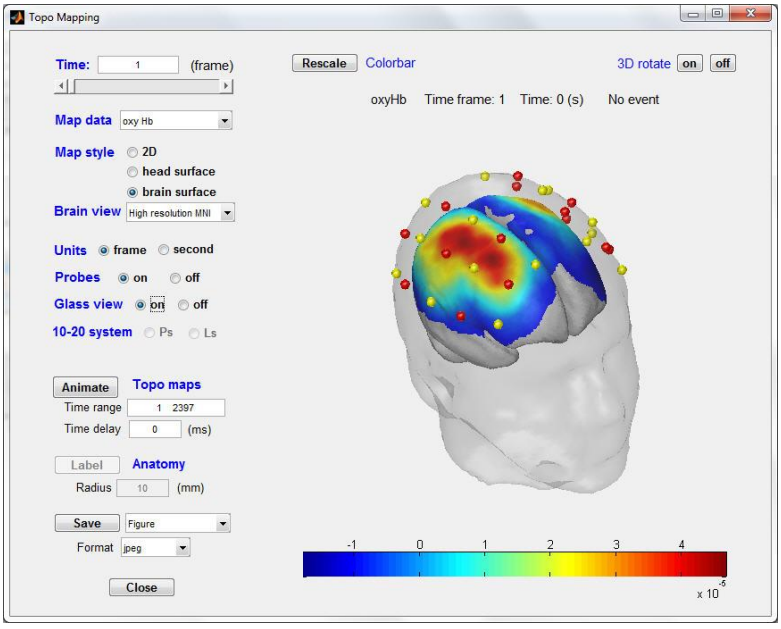


Figure 5-52. An example of glass-viewing.

3.4.4 Overlay EEG 10/10 system montage on head map

When you choose to map the specified hemoglobin data set onto 2D or 3D head surface (*i.e.*, the **2D** or the **head surface** radio button is selected), the two **10-20 system** radio buttons: **Ps** (Positions) and **Ls** (Labels) are enabled. Clicking the **Ps** radio button next to the words **10-20 system**, you can see that all EEG 10-20 system positions are marked on the topographic head map in small blue dots in 2D case and small green dots in 3D case. If you select both **Ps** and **Ls** radio buttons, you can see all 10-20 system positions and their labels on the map. An example of plotting EEG 10-20 system positions and labels on the map is shown here. Clicking the **Ps** radio button, you can see the updated figures in 2D and 3D head surface maps, as shown in Figures 5-53 and 5-54, respectively.

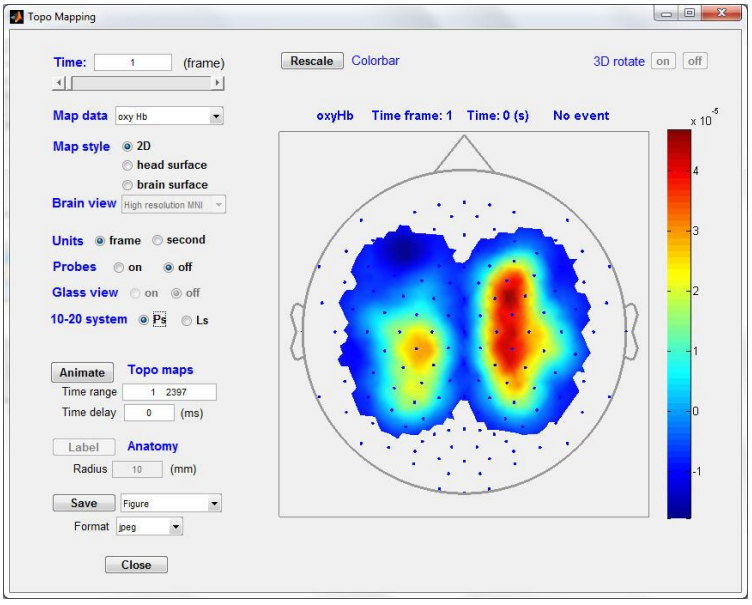


Figure 5-53. The EEG 10-20 system positions mapped on the 2D head surface (blue dots)**.**

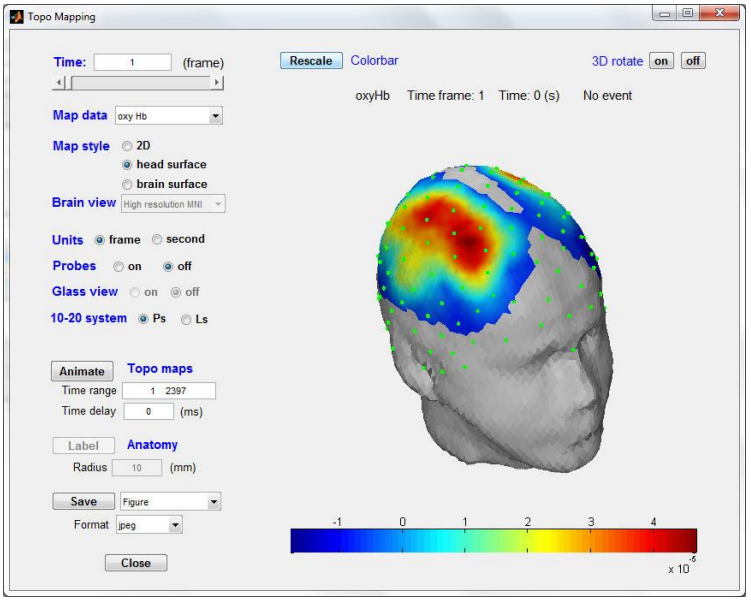


Figure 5-54. The EEG 10-20 system positions mapped on the 3D head surface (green dots)**.**

And clicking both the **Ps** and **Ls** radio buttons, you can see the updated figures in 2D and 3D head surface maps, as shown in Figures 5-55 and 5-56, respectively.

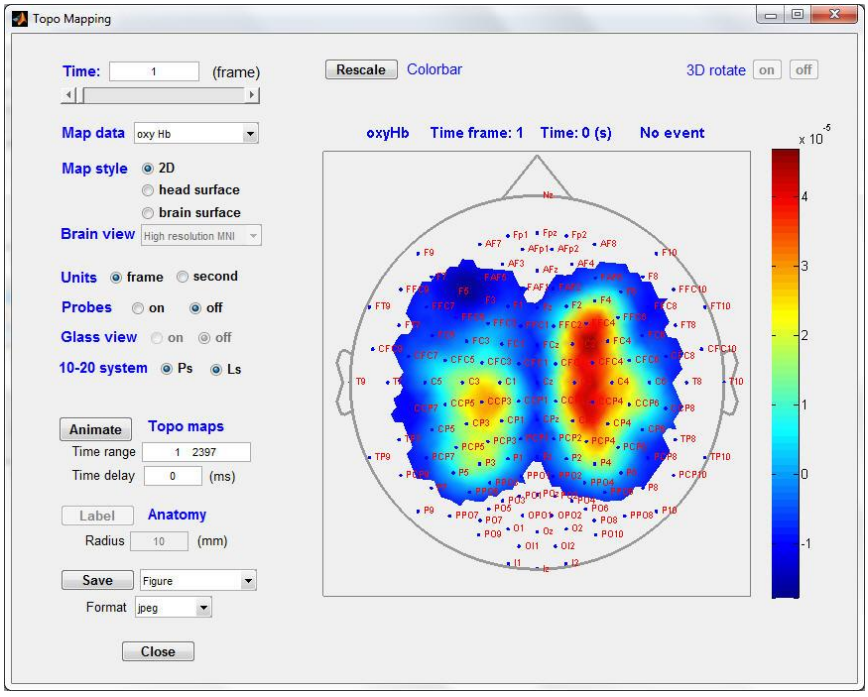


Figure 5-55. The EEG 10-20 system positions and labels mapped on the 2D head surface**.**

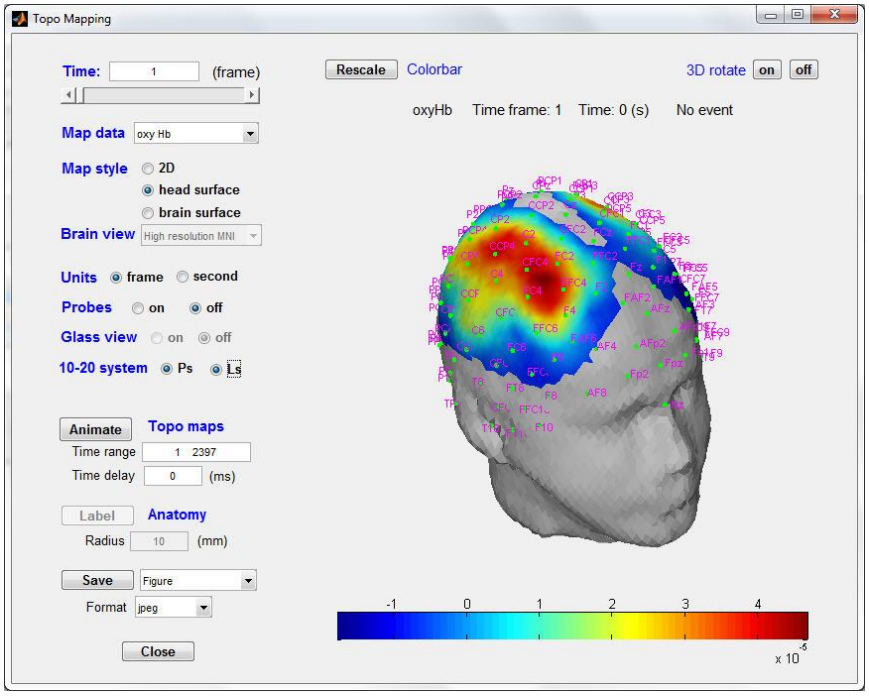


Figure 5-56. The EEG 10-20 system positions and labels mapped on the 3D head surface**.**

3.5 Animating topographic maps

The components in the middle left side of the Topographic Mapping GUI, as shown in highlighted in Figure 5-57, allow you to generate an animation showing the temporal evolution of the specified topographic maps (2D, head surface or brain surface). The components consist of:

Animate push button: for showing the animation;
Time range text field: for selecting the time range for animation;
Time delay text field: for slowing down the movie.

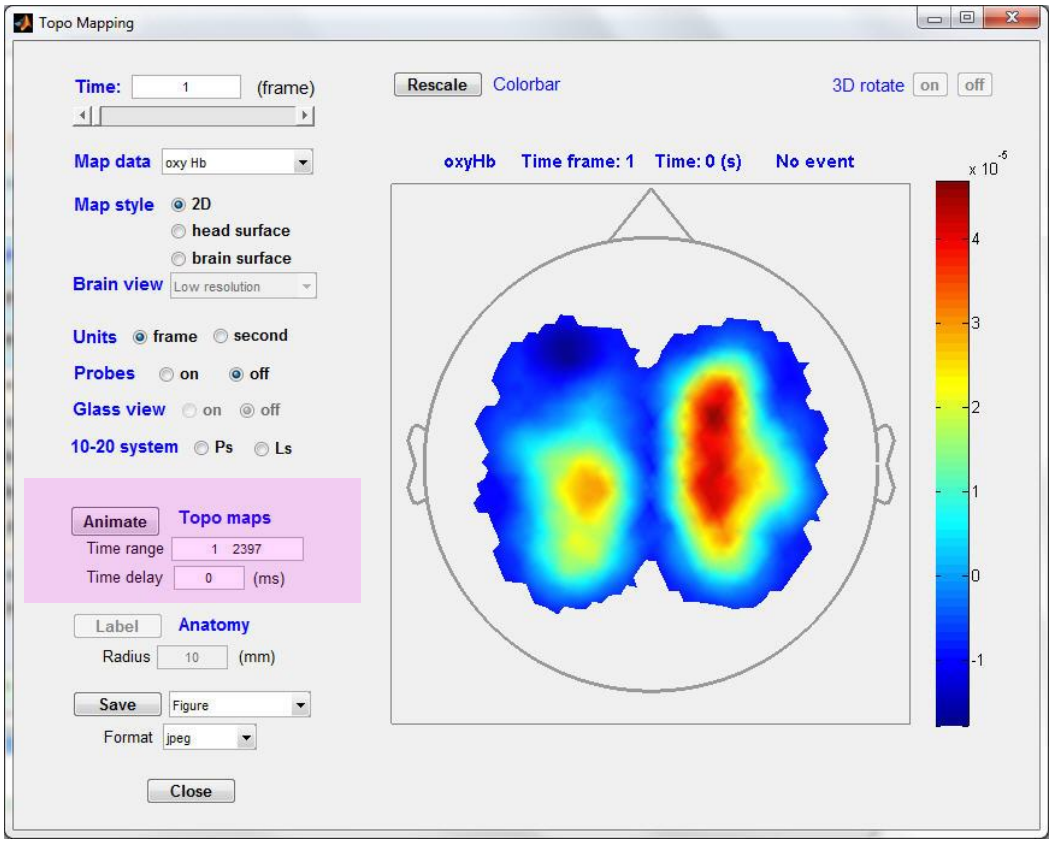


Figure 5-57. Animating topographic maps**.**

Before showing the animation, if you want, you can specify the time range for the movie by typing your desired time range in the **Time range** text field below the **Animate** button. In the text field, the default minimum and maximum values are 1 and the length of the specified hemoglobin hem time series data set, respectively. If you want to slow down the speed of showing the animation, you can type a value (in microseconds) in the **Time delay** text field below the **Time range** text field, then there is time delay after displaying each topographic map during showing the animation. By default, the value in the text field is 0 (ms), *i.e.*, there is no time delay during showing the animation.

An example is shown in the following figure. If you have selected to view the specified hemoglobin time series on brain surface with glass-viewing and plotting probes on the map, clicking the **Animate** button, you can show the specified topographic animation, as shown in Figure 5-58.

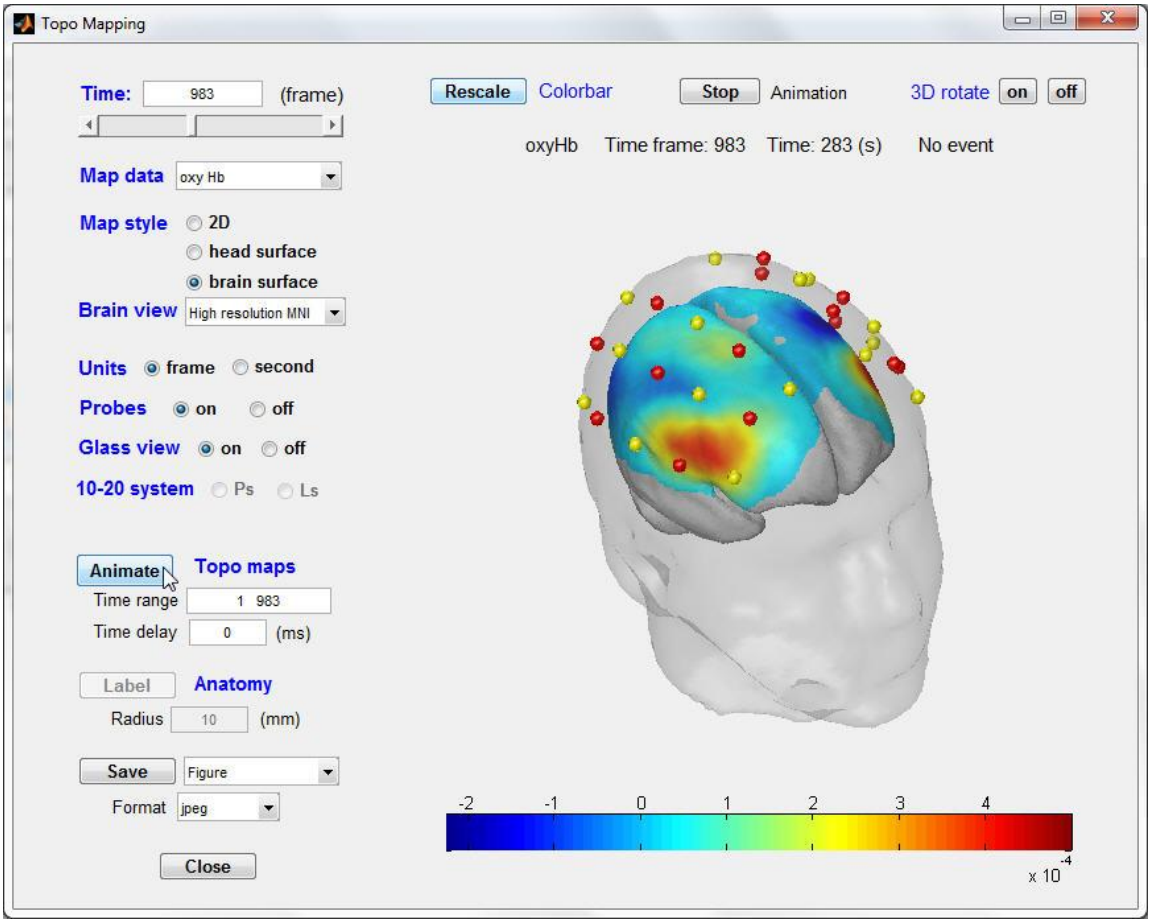


Figure 5-58. An example of animating topographic maps**.**

During showing the animation, a **Stop** Animation button pops up in the middle top of the figure. Clicking the **Stop** button at any time frame/second, you can immediately terminate showing the animation.

3.6 Displaying topographic maps

The components in the right side of the Topographic Mapping GUI, as shown in highlighted in Figure 5-59, allow you to display the specified hemoglobin topographic maps and animation in different color scale and viewing angle. The components consist of:

Axes: for displaying the specified map and animation;

Color bar: for showing the color scale of the map;

Rescale color bar button: for changing the color scale of the map;
3D rotate buttons: for rotating the 3D maps.

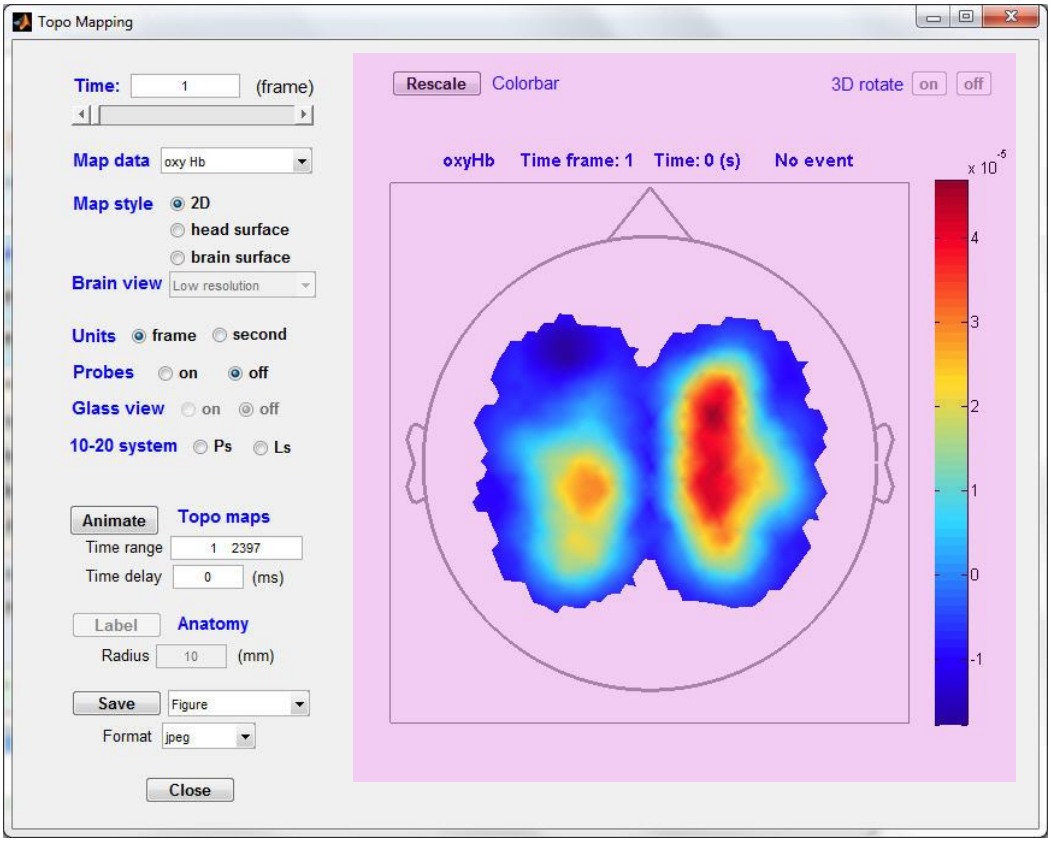


Figure 5-59. Displaying topographic maps**.**

3.7 Adjusting color scale

You can rescale the color scale of the map you are viewing, by using the **Rescale** button prior to the word "Colorbar." By default, each topographic map you specified is color-scaled to its own minimum and maximum values. In contrast, using the **Rescale** button will apply a user-defined color scale to all the maps you are viewing. The following is an example of use of the scaling function for rescaling the color scale of the map.

Step 1: Click the **Rescale** button to open a text field window, where the minimum and maximum values of the color scale of the current map are shown in upper and lower text fields, respectively, as shown in Figure 5-60.

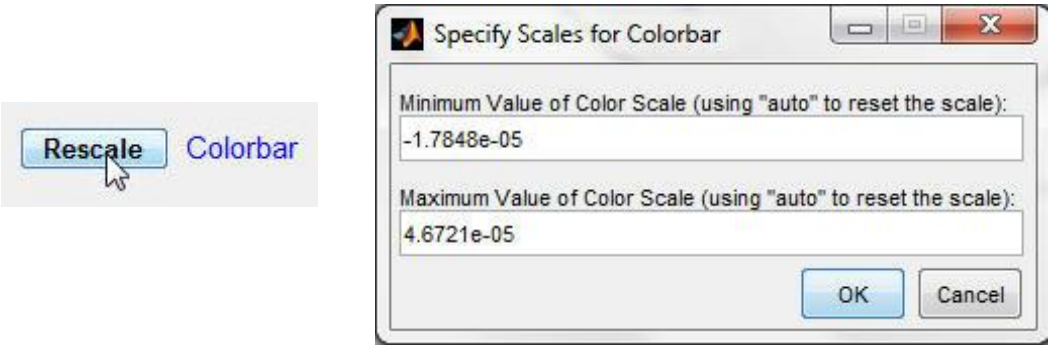


Figure 5-60. Rescaling the color bar**.**

***Step 2*:** Enter the desired minimum and maximum values for the color scale of the map. An example is shown in Figure 5-61.

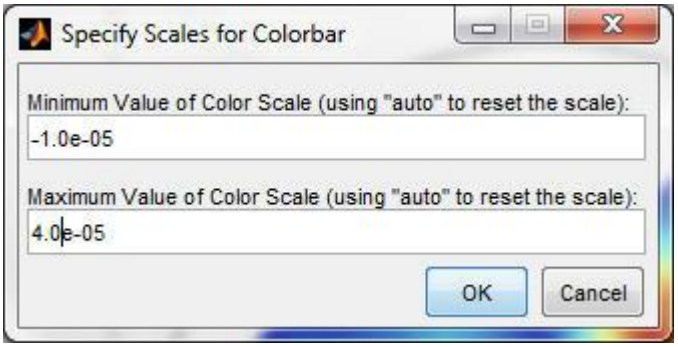

Specify Scales for Colorbar
Minimum Value of Color Scale (using "auto" to reset the scale):
-1.0e-05
Maximum Value of Color Scale (using "auto" to reset the scale):
4.0e-05
OK
Cancel

Figure 5-61. An example of changing the color scale**.**

***Step 3*:** Click the **OK** button to close the text field window. You will see an updated map, with the new color scale, in Figure 5-62:

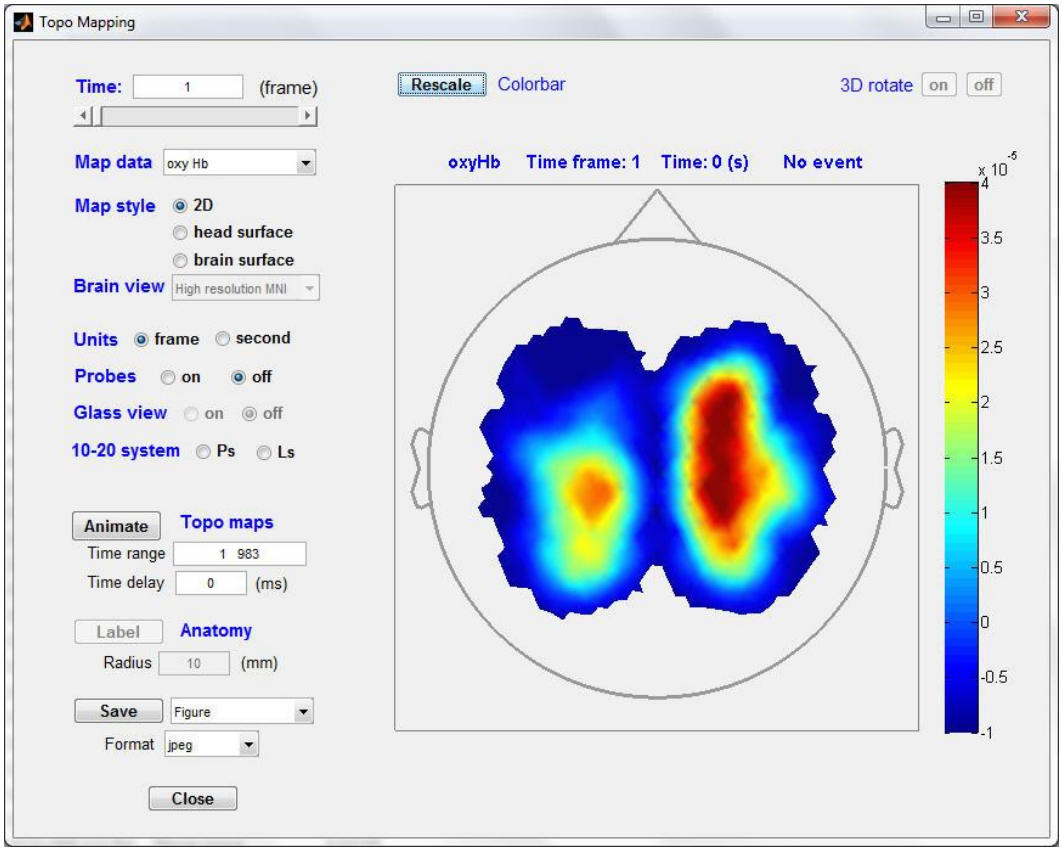


Figure 5-62. The color-rescaled topographic map**.**

***Note*:** You can reset the minimum and maximum values of the color scale to their default values by typing "auto" in the corresponding text fields, as shown in Figure 5-63.

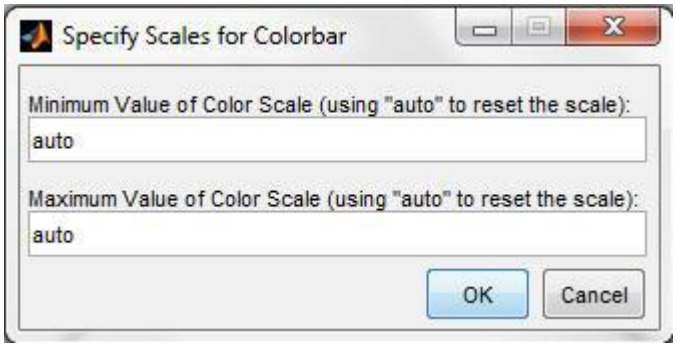

Specify Scales for Colorbar
Minimum Value of Color Scale (using "auto" to reset the scale):
auto
Maximum Value of Color Scale (using "auto" to reset the scale):
auto
OK
Cancel

Figure 5-63. Reset the color scale to the default values**.**

3.8 Rotating 3D map

When you select to map the specified hemoglobin data set onto 3D head surface or brain surface (*i.e.*, the **head surface** or **brain surface** radio button is selected), two 3D rotation button: **on** and **off** in upper

right corner of the GUI are enabled. Using these two buttons, you can rotate the 3D map by moving mouse. To do this, click the **on** button next to the words "3D rotate," move the mouse cursor onto the topographic map, press and hold down the primary mouse button, and rotate the map by moving the mouse. Figure 5-64 shows an example of rotating the map.

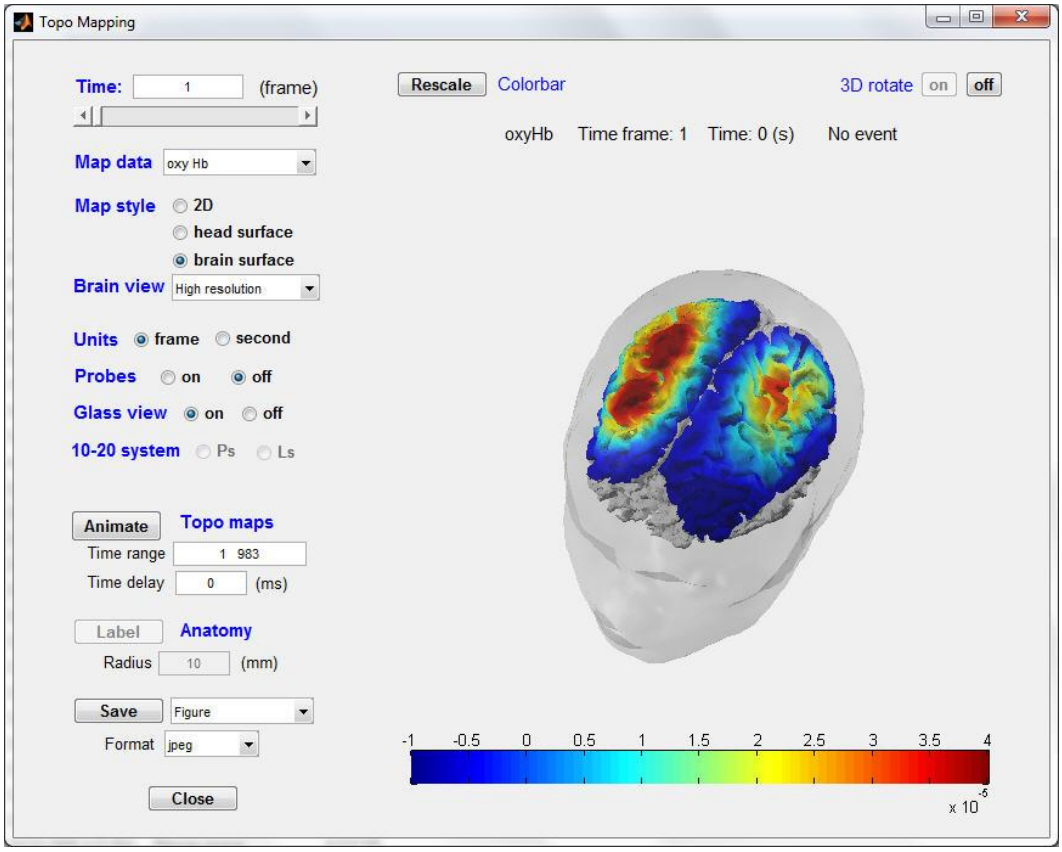


Figure 5-64. An example of rotating the 3D map**.**

***Note*:** Once you chose a desired viewing angle by rotating the map, you had better click the **off** button next to the **on** button to turn off the image rotation function and to fix the viewing angle in the GUI.

3.9 Saving topographic map and animation

The components in lower left side of the Topographic Mapping GUI, as shown in highlighted in Figure 5-65, allow you to export the specified hemoglobin topographic maps and animation for future uses. The components consist of:

Save button: for exporting the specified map or animation;
Two pull-down menu: for saving choices (map or animation, formats).

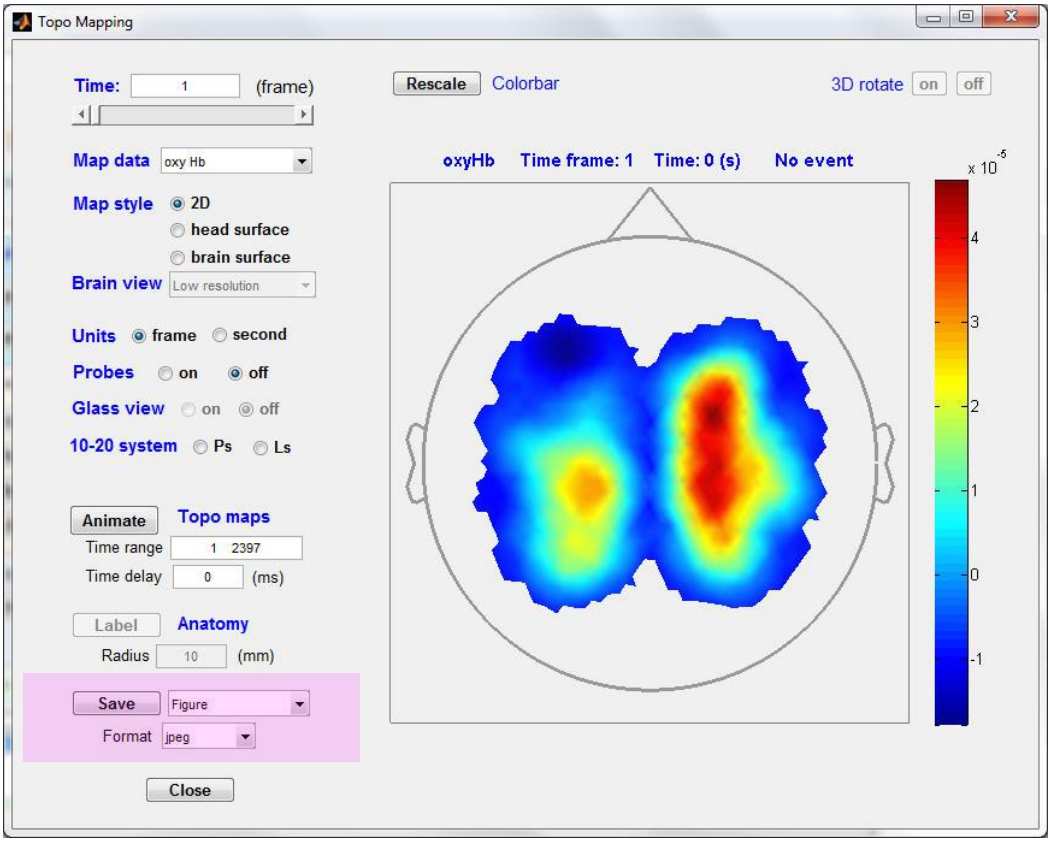


Figure 5-65. Saving topographic map and animation**.**

3.9.1 Saving topographic map

Following the steps below, you can save the topographic map that is currently displayed in the Topographic Mapping GUI.

Step 1: Click the pull-down menu next to the **Save** button, and select the first option (Figure) in the menu (this is the default case), as shown in Figure 5-66.

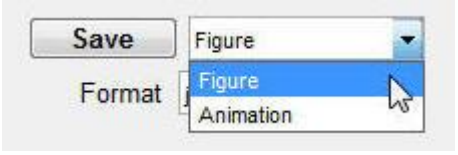


Figure 5-66. Saving topographic map**.**

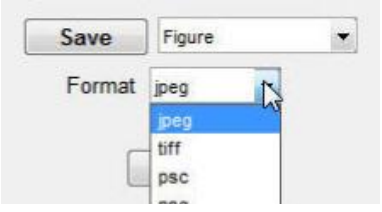


Figure 5-67. Specifying the saving figure format**.**

***Step 2*:** Click the **Format** pull-down menu below the **Save** button, and select one of the figure formats you want in the menu, as shown in Figure 5-67.

***Step 3*:** Click the **Save** button to open a browser window for saving the map, as shown in Figure 5-68.

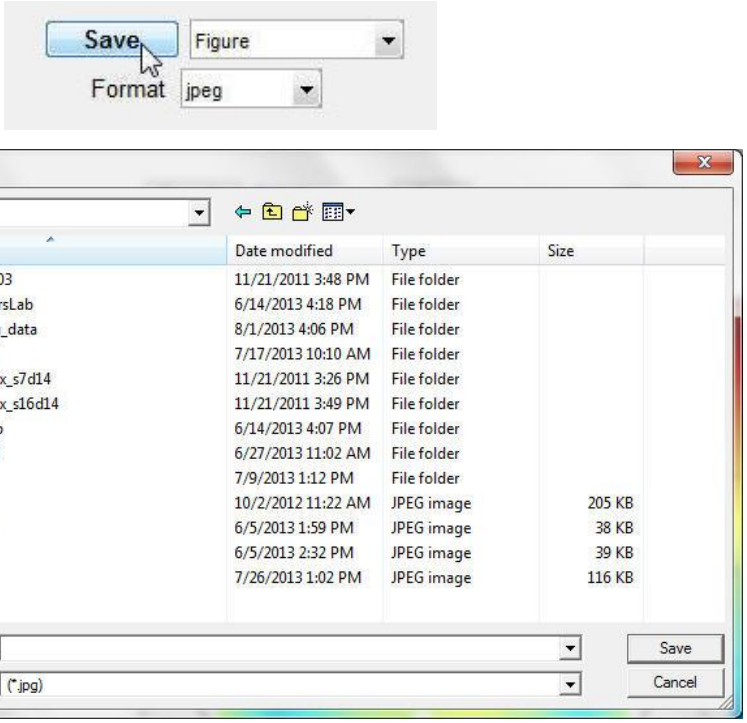


Figure 5-68. Specifying the file name and folder for the saving figure**.**

***Step 4*:** Use the browser window to navigate to the folder where your selected map will be saved in, type a desired file name in the **File name** field, then click the browser window **Save** button to store the map.

3.9.2 Saving animation

Following the steps below, you can save the animation that you have viewed in the Topographic Mapping GUI.

***Step 1*:** Click the pull-down menu next to the **Save** button, and select the second option (Animation) in the menu, as shown in Figure 5-73.

Figure 5-69. Saving animation**.**

***Step 2*:** Click the **Save** button to open a text field window for selecting an animation format and playback rate of the saving animation, type 1 (the animation will be saved in avi format) or 2 (saved in mp4 format) in upper text field, and type a value you desire as the rate of playback of the saving animation (in frames per second) in lower text field, as shown in Figure 5-70.

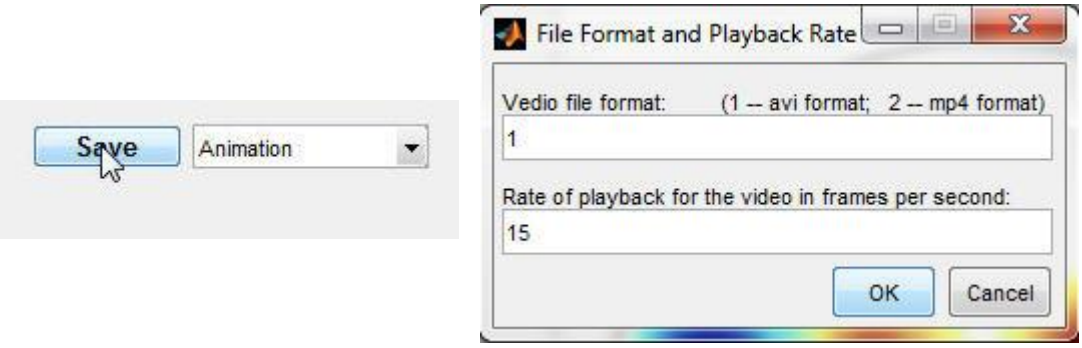


Figure 5-70. Specifying the saving animation format and the playback rate.

***Step 3*:** Click the **OK** button in the text field window to open a browser window for saving the animation, as shown in Figure 5-71.

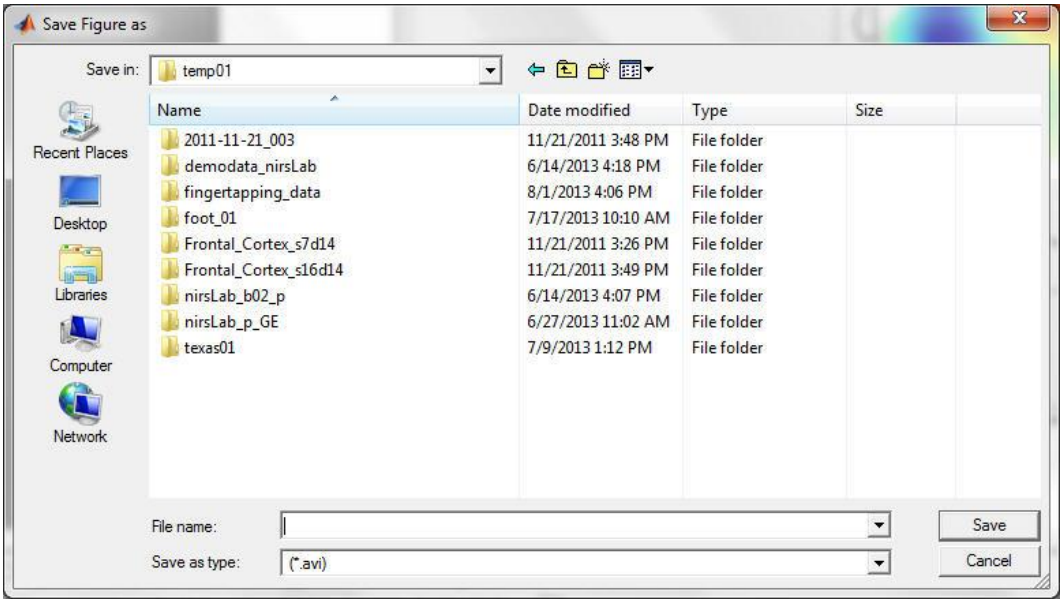


Figure 5-71. Specifying the file name and folder for the saving animation**.**

***Step 4*:** Use the browser window to navigate to the folder where your selected animation will be saved in, type a desired file name in the **File name** field, then click the browser window **Save** button to store the animation.

4 Map Hemodynamic States: block averaged states

After you click the pull-down menu following the words **Hemodynamic states** and select the option of **Block averaged,** pressing the **Map** Hemodynamic States button will open a progress bar to show the process of initializing the mapping data, then, a few seconds later, will bring up a new GUI named Topographic Mapping: Block averaged states, as shown in Figure 5-72, which allows you to topographically map the block-averaged hemoglobin images onto head and brain surfaces.

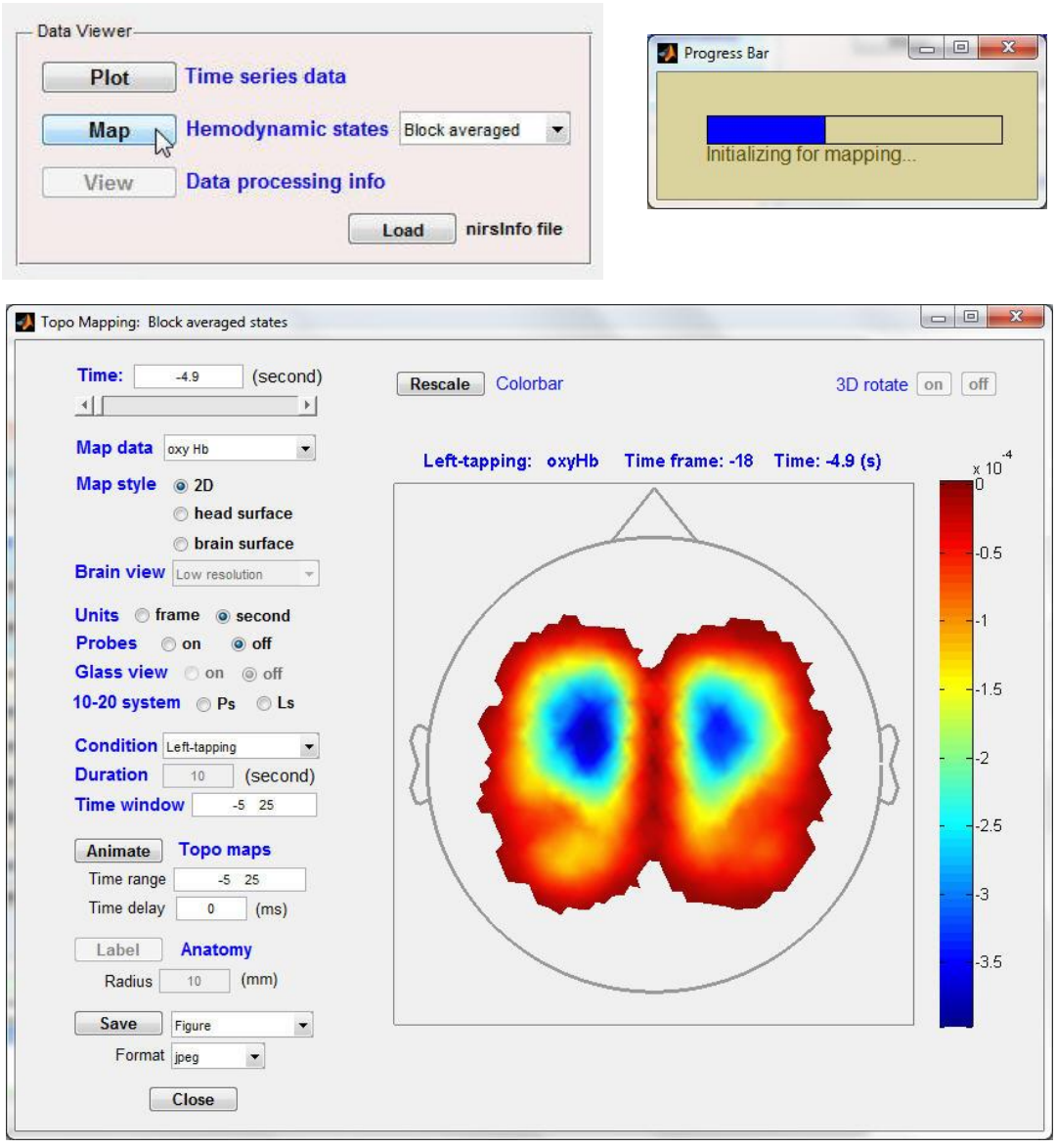
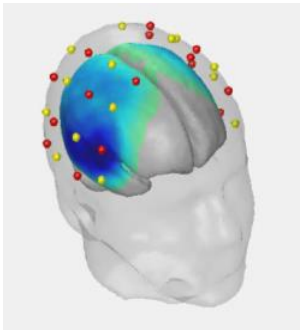
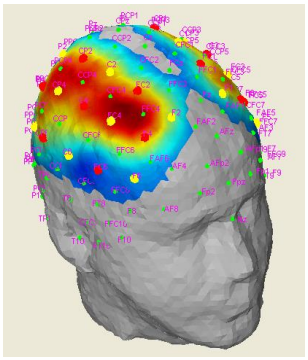
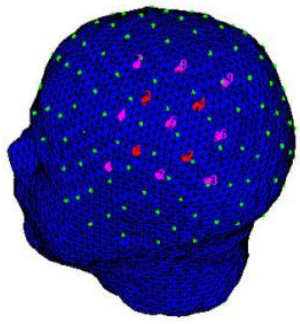
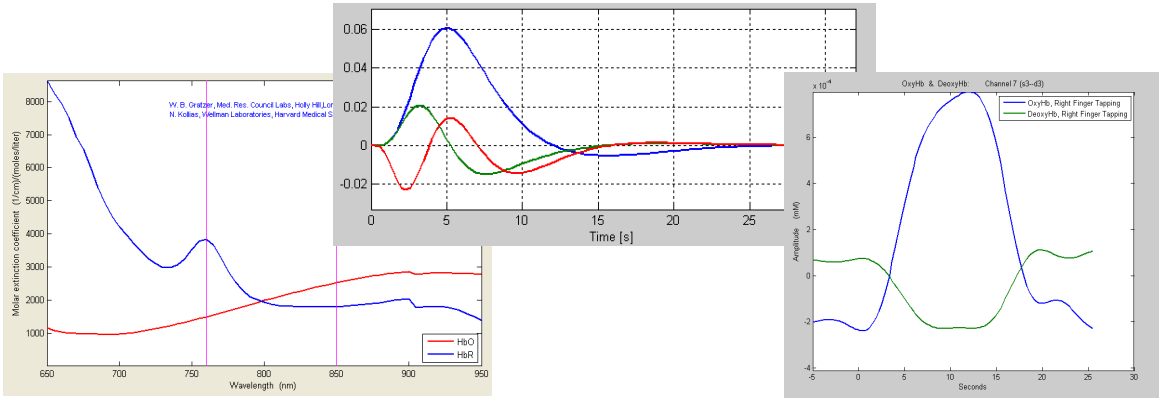


Figure 5-76. Mapping the block-averaged hemodynamic states and the Topographic Mapping GUI**.**

Comparing the topographic mapping GUI for block-averaged hemodynamic states (Figure 5-72) with the GUI for all hemodynamic states (Figure 5-36), we can find that the only difference is that there are three more controls in the former, as shown in Figure 5-73, which allow you to specify different conditions and time window for the mapping block-averaged states. So you can follow the guidance described in last section to use the GUI to map the block-averaged images onto head and brain surfaces.

Figure 5-73. The controls for block-averaged states in the Topographic Mapping GUI**.**

nirsLAB

Chapter 6: Data Analysis

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1 Introduction

The *Data Analysis* portal uses functions found in the SPM (Statistical Parametric Mapping) freeware package to extend the capabilities of nirsLAB to include statistical analysis of hemodynamic-state time series. Several of the currently favored techniques for interpretation of neuroimaging data collected during designed experiments are available at this time, for both Level-1 (within-session and within-subject) and Level-2 (across multiple sessions or subjects) analyses. The functions currently available include:

- Level-1 general linear model (GLM) analysis of fNIRS hemodynamic-state time series, to evaluate the position-dependent relationships between computed data-channel responses (Chap. 4) and user-specified temporal models.
- Level-1 and Level-2 assessment of the statistical significance of the GLM model-fitting coefficients (t-test, ANOVA), or of user-defined contrasts of two or more models.

When you launch the nirsLAB application, the primary GUI (Chap. 1, Figure 1) opens with the buttons in the *Data Analysis* portal already enabled, as shown in Figure 6-1. The reason for this setting is that it allows you to re-visit sets of hemodynamic-states data that were

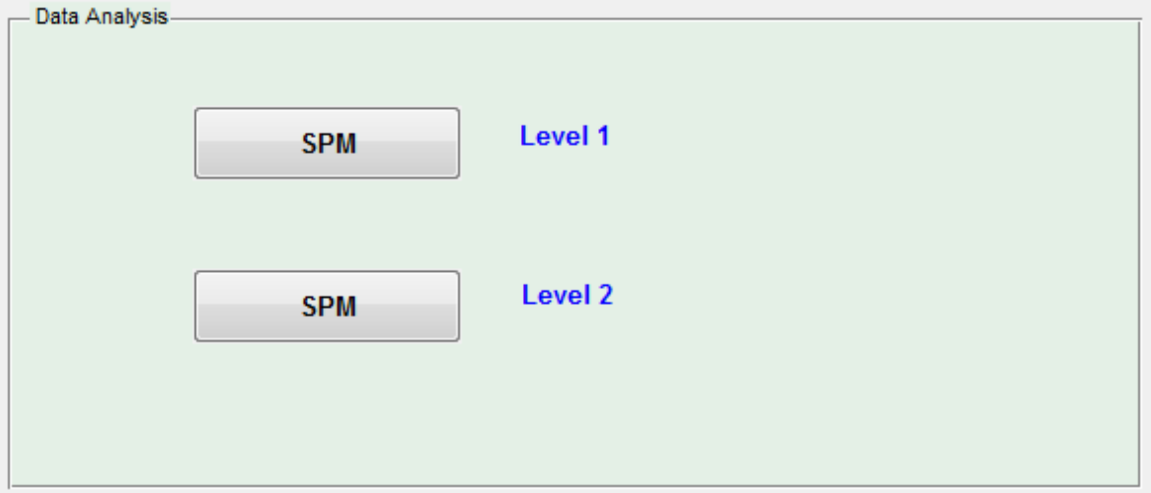

Figure 6-1. The *Data Analysis* portal, as it appears at nirsLAB

generated in previous nirsLAB sessions, and to perform statistical analyses on them in the current session. Consequently, you can click on either button at any time, to launch one of the GUIs shown in Figure 6-2. However, nirsLAB will not allow you to proceed beyond that initial step if you try to analyze data for which you haven't yet performed a hemodynamic-states computation (see Figure 6-4, in Section 2.1).

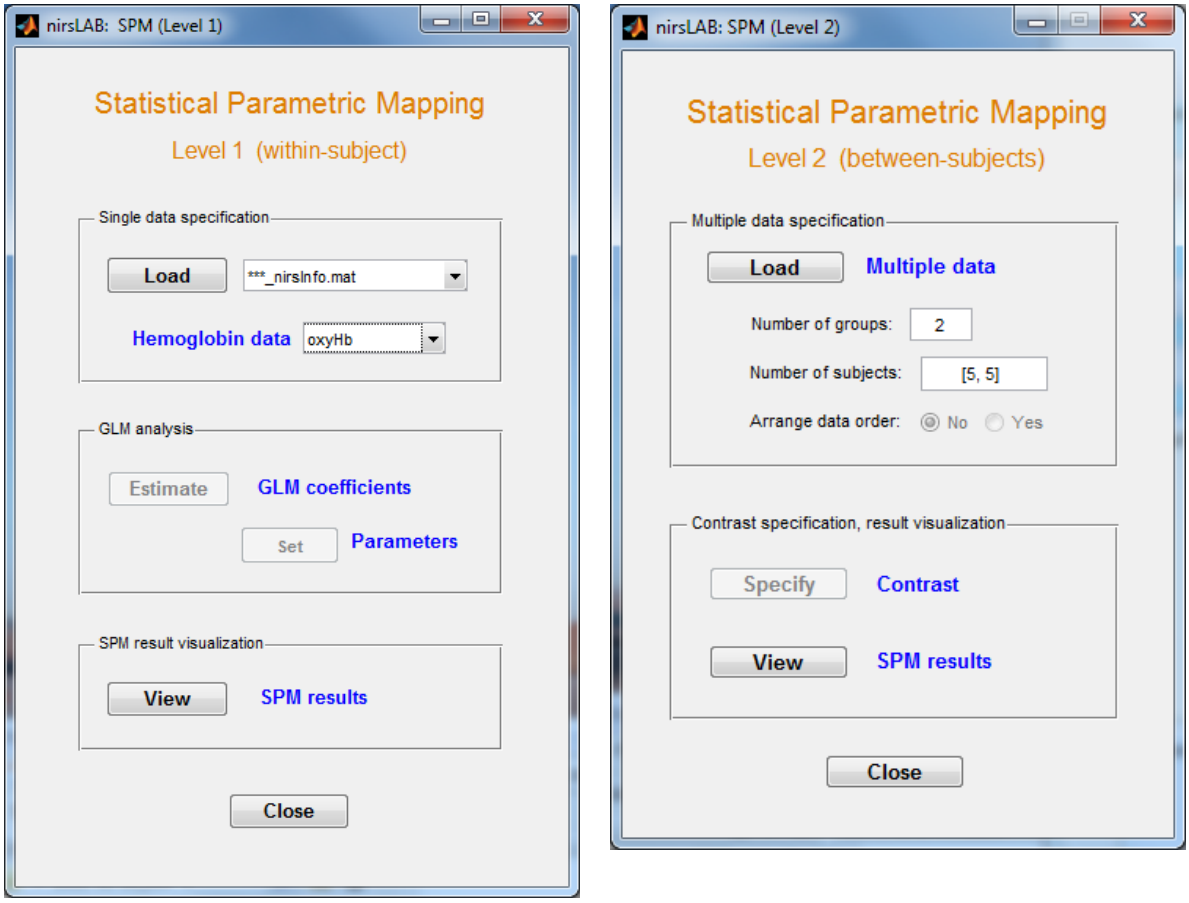

Figure 6-2. (Left) Default appearance of the GUI that you can launch by clicking on the *SPM Level 1* button of the *Data Analysis* portal (see Section 2). (Right) Default appearance of the GUI that you can launch by clicking on the *SPM Level 2* button of the *Data Analysis* portal (see Section 3).

2 SPM Level 1

2.1 'Single data specification' module

You may find that most commonly you will proceed directly from initializing a project to preprocessing, computation of hemodynamic states, and analysis. However, we have made a point of designing nirsLAB so that you are not required to get all the way through the processing sequence in a single sitting, and so that you can return to projects that you initialized at any time in the past. In order to achieve this flexibility, you are required to always specify which data set you want to analyze. Therefore, the first step in Level-1 SPM is to make a selection from the drop-down menu, shown enlarged in Figure 6-3, to the right of the *Load* button (Figure 6-1). Select the 'Pre-defined Hb dataset' option if you want to view results from a GLM computation that you have already performed. Otherwise, select the default '***_nirsInfo.mat' option and, from the items in the second menu shown in Figure 6-3, specify the hemodynamic state that you are interested in. Then click on the *Load* button. A browser window will pop open, for you to use

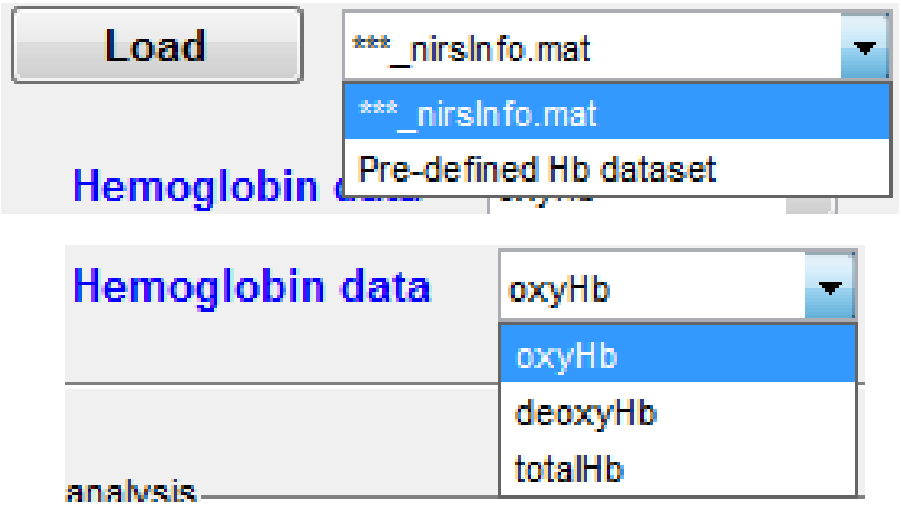

Figure 6-3. Detail views of the drop-down menus in the 'Single data specification' module of the *Statistical Parametric Mapping Level 1 (within subject)* GUI (Figure 6-2).

to navigate to your nirsInfo file (if you have selected the '***_nirsInfo.mat' menu item) or previously generated SPM output file (if you have selected 'Pre-defined Hb dataset') of interest. If you load a nirsInfo file, and the previously performed processing steps do not include computation of hemodynamic states (Chap. 4), then nirsLAB will produce a pop-up message (Figure 6-4) reminding you of the necessity for performing a hemodynamic-states computation before you can proceed to GLM analysis.

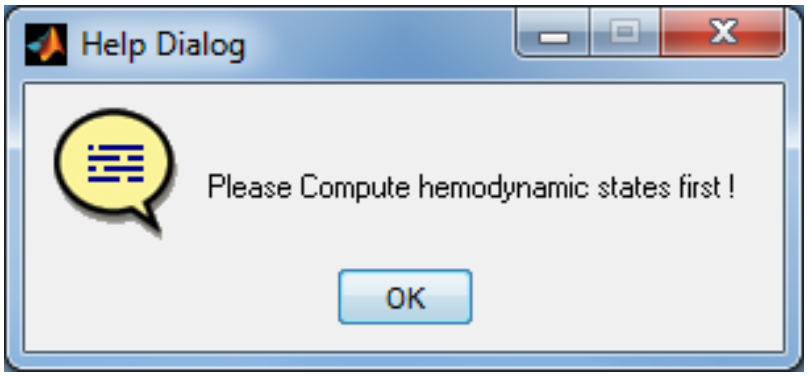

Figure 6-4. Pop-up message generated by nirsLAB if the user loads a nirsInfo file, in the *Statistical Parametric Mapping Level 1 (within subject)* GUI (Figure 6-2), for a project that doesn't have hemodynamic-states data.

- If you have selected '***_nirsInfo.mat', then navigate to a folder containing a nirsInfo file and load that file. In response, nirsLAB will create a folder named 'nirsSPM', containing a sub-folder named 'nirs_data', in that same location (This assumes that folders with these names do not already exist there. If they do, nirsLAB takes no action.) A browser window will open, for you to use to specify a name and location for the files that the SPM computation will generate.

- The first new file contains a copy of the time series for the hemodynamic state that you selected from the 'Hemoglobin data' menu (Figure 6-3). As shown in Figure 6-5, the 'nirs_data' sub-folder is its default location, and the nirsLAB-suggested file name contains the selected hemodynamic state and the common root of the project-specific data files. (You are free to choose a different location and/or name if you like.) After you click on the *Save* button highlighted in Figure 6-5 (blue oval), nirsLAB will produce a pop-up message confirming the location and name of the saved file (Figure 6-6).

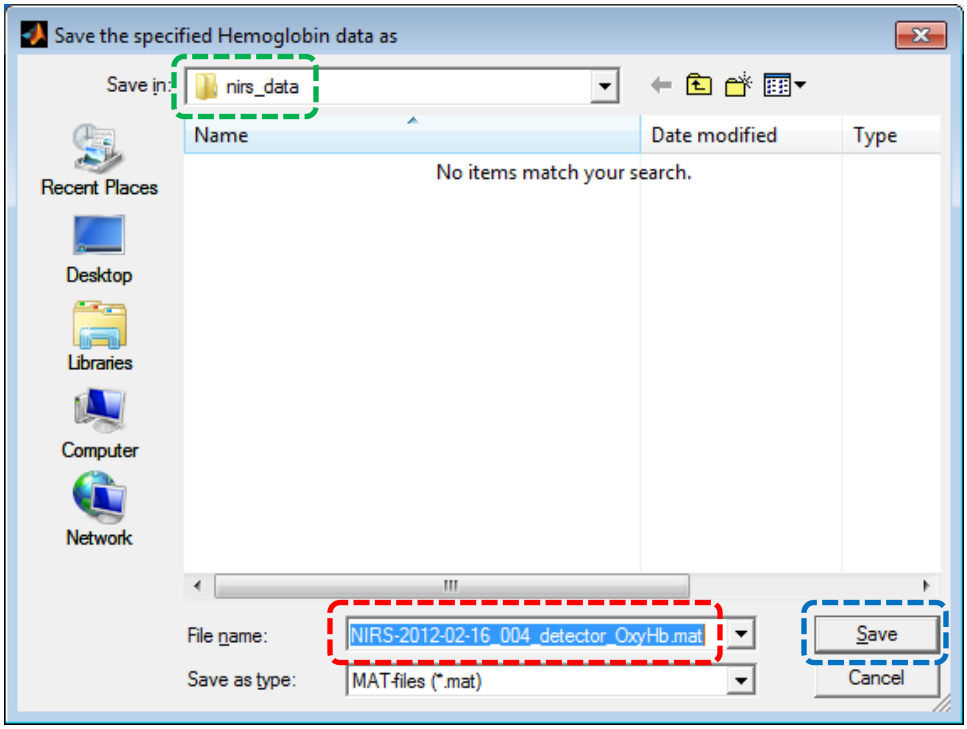

Figure 6-5. An example of the browser window that open after a nirsInfo file is loaded. The nirsLAB-suggested name (red oval) and location (green oval) for the first output file are highlighted. In this example, the common root of the demo dataset is 'NIRS-2012-02-16_004' and the oxygenated hemodynamic state was selected from the 'Hemoglobin data' menu (Figure 6.3).

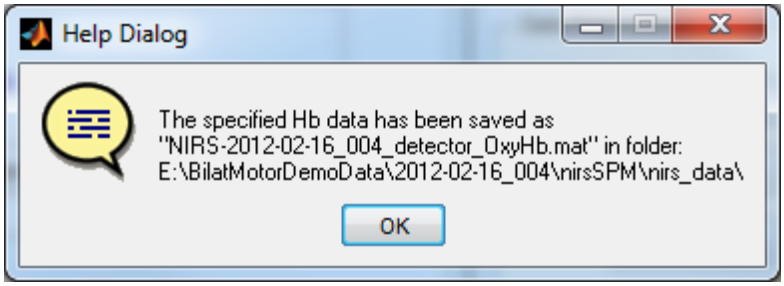

Figure 6-6. Pop-up message generated by nirsLAB, after the reformatted hemodynamic-state data file is created, confirming the file name and location.

- When the GLM computation is complete, nirsLAB will create a second sub-folder, named 'spm_results', inside the 'nirsSPM' folder (unless there already is a sub-folder with that name, in which case no action is taken). This is the default location for all of the files that contain GLM-computation results (see Section 2.2).

- If you have selected 'Pre-defined Hb dataset' (*i.e.*, an appropriately reformatted file, such as the NIRS-2012-02-16_004_detector_OxyHb.mat example shown in Figure 6-5, already exists), then navigate to the folder where the file containing the data you want to analyze is stored, select it, and click on the *Open* button, as depicted in Figure 6-7. In response, nirsLAB will produce a pop-up message confirming that the file you specified was successfully loaded (Figure 6-8).

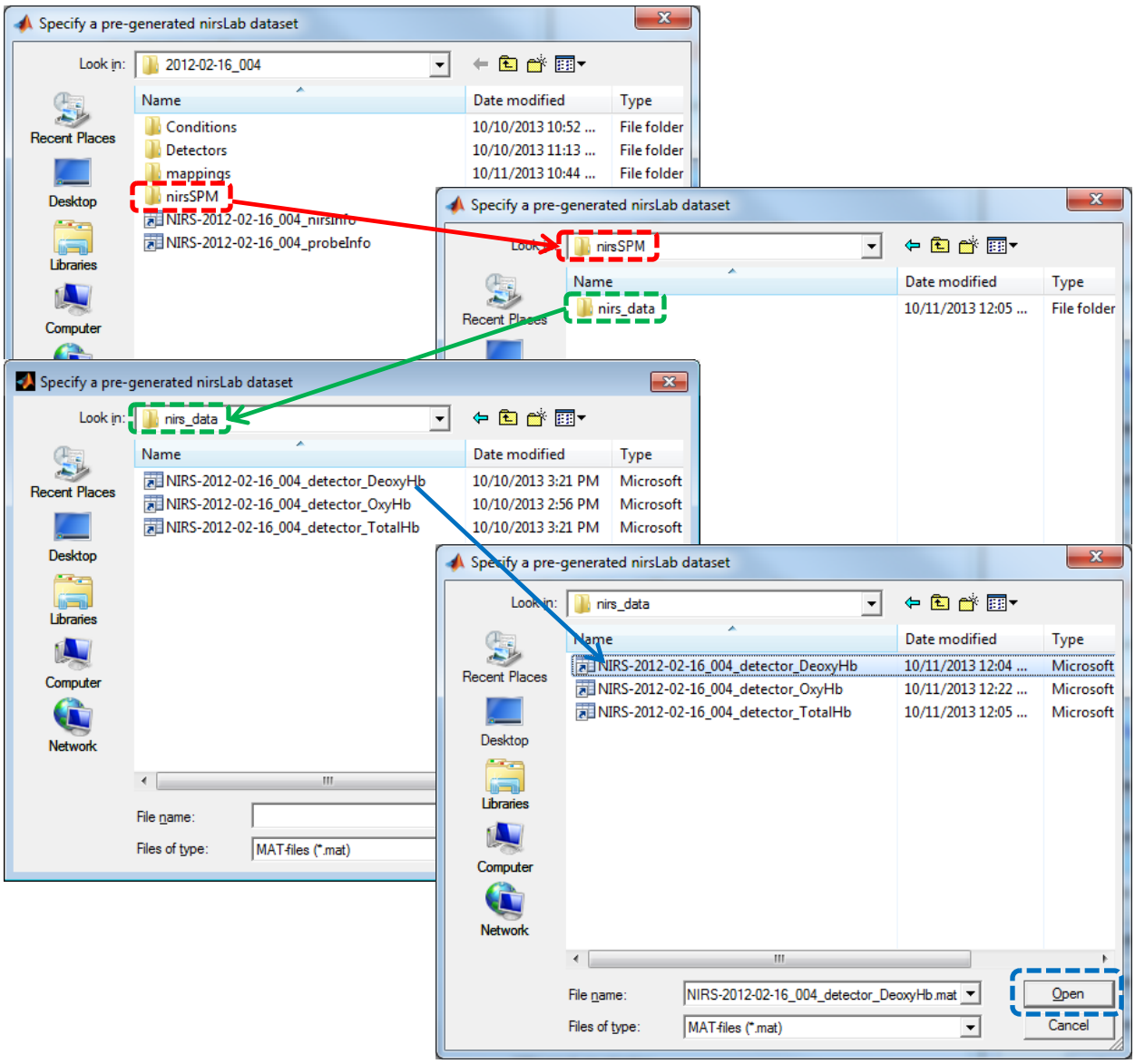

Figure 6-7. An example of the process of navigating to a folder that contains files of hemoglobin-state data formatted for Level-1 SPM, and selecting one for analysis.

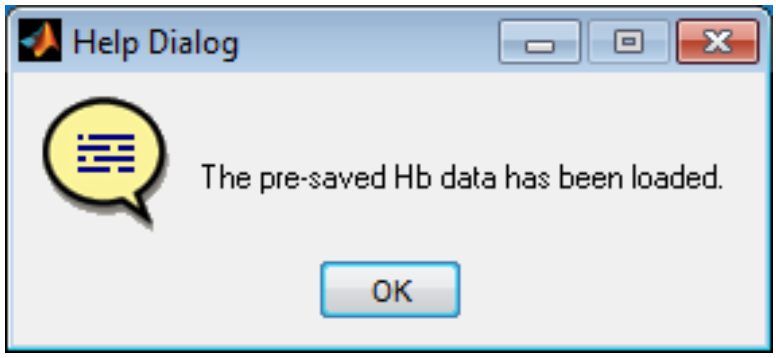

Figure 6-8. Pop-up message generated by nirsLAB after a SPM-formatted hemodynamic-state data file is loaded.

When a valid file has been loaded, using either of the preceding methods, the *Set Parameters* button becomes enabled in the 'GLM analysis' module of the *Statistical Parametric Mapping Level 1 (within subject)* GUI (Figure 6-2), as illustrated in Figure 6-9. You may now proceed to the steps described in Section 2.2.

Figure 6-9. The 'GLM analysis' module of the ***Statistical Parametric Mapping Level 1 (within subject)*** **GUI** (Figure 6-2) after specification of a dataset. The *Set Parameters* button is now enabled.

2.2 'GLM analysis' module

2.2.1 Setting Parameters

Click on the *Set Parameters* button shown in Figure 6-9 to launch the *Parameter Setup for GLM Analysis (Level 1)* GUI shown in Figure 6-10. The 'Data Information' module, shown enlarged in Figure 6-11, has several fields containing (grayed out) information extracted from the file that you selected in the 'single data specification' step. We recommend that you make a point of examining the contents of these fields to confirm that you have chosen the dataset that you intended. In the 'Directory for GLM results:' line of the 'Data Info' module, nirsLAB supplies a default location for the output of the SPM computations. If you want the output to go somewhere else, select the 'User-defined' option from the drop-down menu. This will cause a

browser to pop up, which you can use either to navigate to an existing folder or to create a new one.

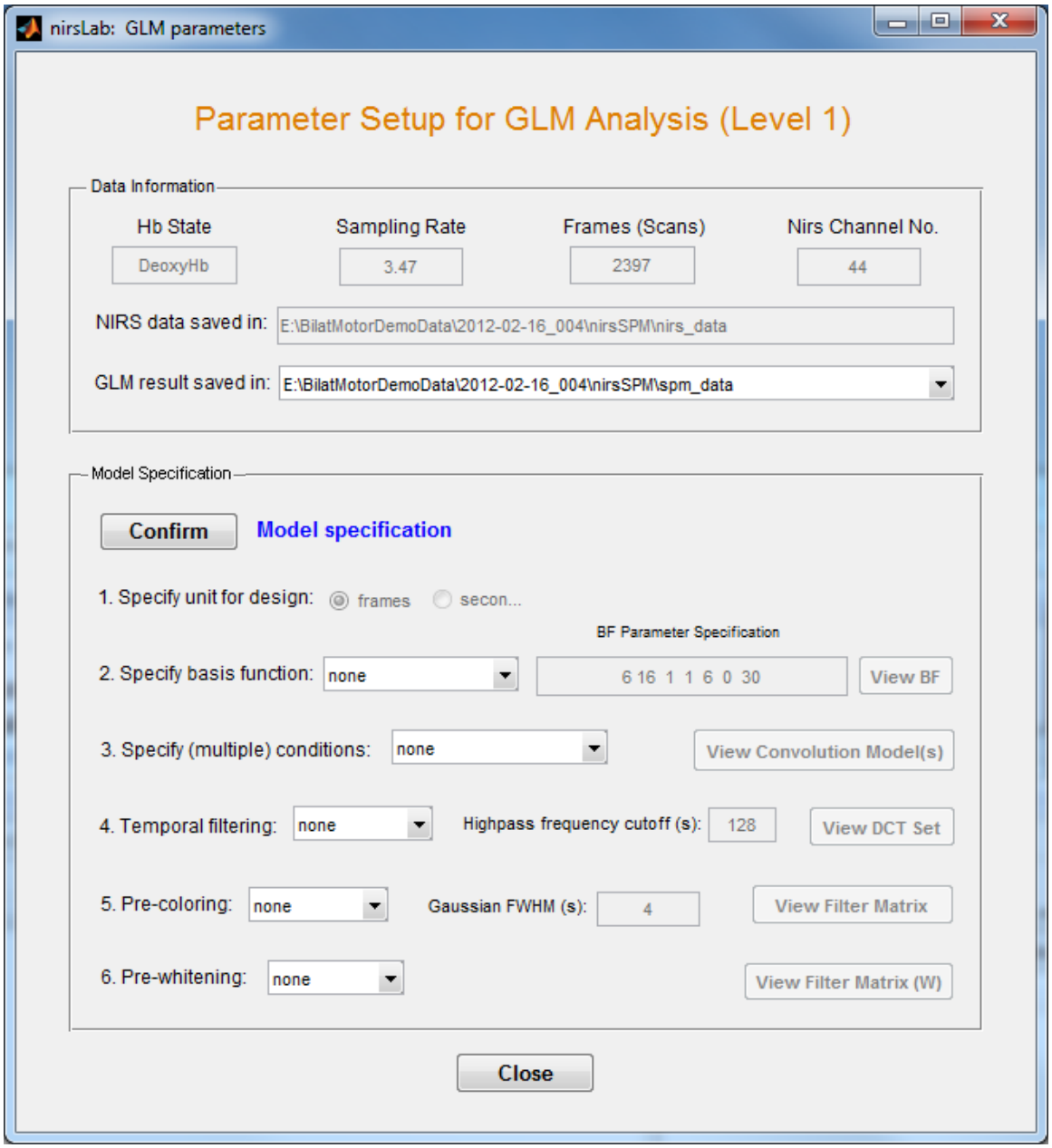

Figure 6-10. The *Parameter Setup for GLM Analysis (Level 1)* GUI, which is launched when you click on the *Set Parameters* button in the 'GLM analysis' module (Figure 6-9) of the *Statistical Parametric Mapping Level 1 (within subject)* GUI (Figure 6-2).

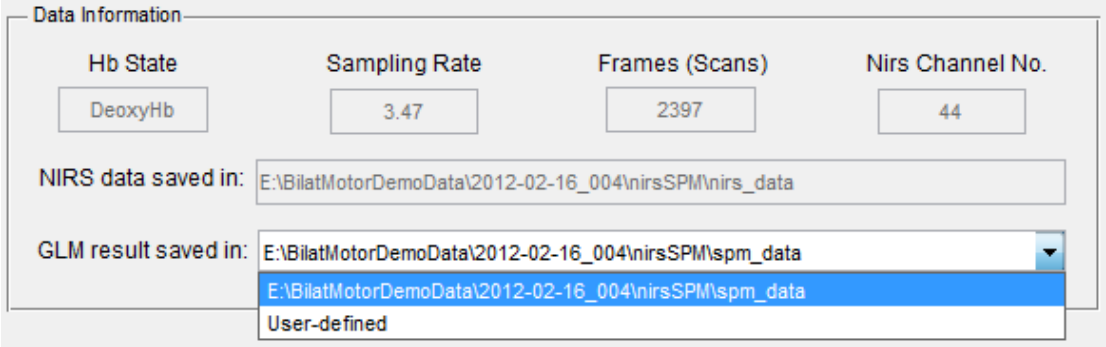

Figure 6-11. Detail views of the drop-down menus in the 'Data Information' module of the *Parameter Setup for GLM Analysis (Level 1)* GUI (Figure 6-10).

Note that there are six control parameters listed in the 'Model Specification' module of the *Parameter Setup for GLM Analysis (Level 1)* GUI (Figure 6-10). However, the first of these, 'Specify unit for design:', is grayed out in the current release of nirsLAB. Thus it is necessary, for the time being, that you use measurement frames as the time unit when you specify the duration of the hemodynamic response function (as described in the next paragraph). Subsequent revisions of nirsLAB will allow you to choose seconds instead, and will ensure that your time-unit selection is applied consistently across all of the user-specified parameters in the 'Model Specification' list. The significance of, and instructions for, the remaining items in the 'Model Specification' list are:

'Specify basis function:'. The basis function is a mathematical model that you use to account for the physiological fact that the hemodynamic response to a change in neural activity is not perfectly synchronized with that activity. If a person is, for example, presented with a brief flash of light as a visual stimulus, his primary visual cortex activity will increase immediately but the resulting in-rush of oxygenated blood to that region typically begins 1-2 seconds later, peaks at ~6 sec after stimulus onset, and persists for a few tens of seconds. Therefore it is recommended that you select a basis function other than 'none' for your data analyses. (However, you may find that 'none' is useful for testing, training and demonstration purposes.)

Before you choose an item from the 'Specify basis function:' drop-down menu, the 'BF Parameter Specification' field and *View BF* button are grayed out. They become enabled when you select any item other than the default 'none' from the menu. Figure 6-12 illustrates what happens when you select the 'hrf' item from the menu. You will notice that there are seven values in the number field, and that the wording of the header changes to 'HRF Parameter Specification'. (As shown in Figures 6-13 through 6-17, selecting other menu items produces different numbers of parameters and different headers.) If you now click on the *View BF* button, the graphics window shown in Figure 6-12 will pop open. The curve plotted here is a "canonical **h**emodynamic **r**esponse **f**unction," and you can see that it exhibits the qualities described in the preceding paragraph: values noticeably greater than zero start about one second after the event onset at 'Time [s]' = 0, the maximum value occurs about five seconds post-onset, and there is a gradual decay back to the baseline.

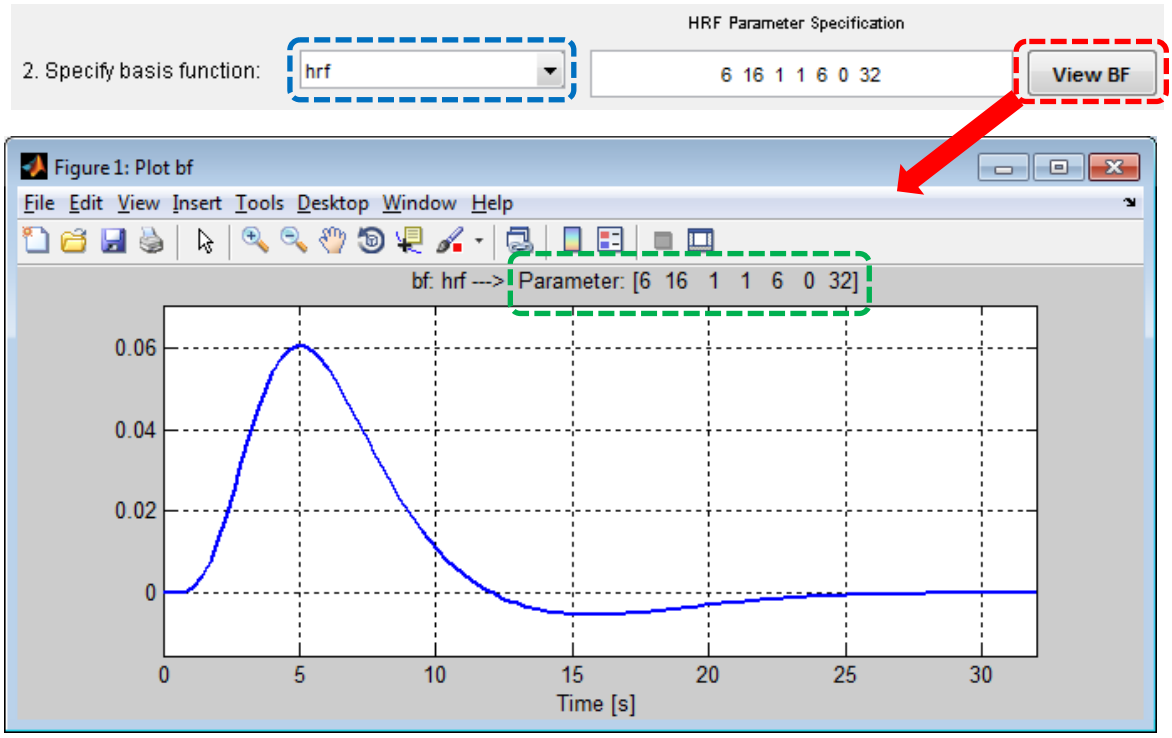

Figure 6-12. (Top) Detail view of the changes, produced by selecting 'hrf' in the drop-down menu (blue oval), seen in the 'Specify basis function:' row of the 'Model Specification' module of the *Parameter Setup for GLM Analysis (Level 1)* GUI (Figure 6-10). (Bottom) Clicking on the *View BF* button (red oval) produces a pop-up plot of the canonical hemodynamic response function corresponding to the default user-specifiable parameters (green oval).

The numerical values assigned to the parameters influence features such as the time to maximum and minimum value and the dispersion (width) of the positive- and negative-going peaks. Because of interactions between the parameters' effects, there isn't a direct correspondence between any one of them and a specific feature such as the time-to-peak or the peak width. Even so, each parameter has a primary role in shaping the overall response function. These are:

- Parameter 1 (default value = 6) is the principal determinant of the time (in seconds) at which the response reaches its maximally positive value. Increasing its value increases the time-to-peak.
- Parameter 2 (default value = 16) is the principal determinant of the time (sec) at which the response reaches its maximally negative value. Increasing its value increases the time-to-trough.
- Parameter 3 (default value = 1) is the principal determinant of the width (sec), or "dispersion," of the positive-going peak.
- Parameter 4 (default value = 1) is the principal determinant of the dispersion (sec) of the negative-going peak.

- Parameter 5 (default value = 6) is approximately equal to the ratio (dimensionless) of the maximum positive value to the (absolute value of the) maximally negative value. The approximation gets better as the time interval between the maximum and minimum values increases.
- Parameter 6 (default value = 0) is the time lag (sec) between the onset of the experimental condition (*i.e.*, 'Time [s]' = 0) and the start of the associated hemodynamic response.
- Parameter 7 (default value = 32) is the total duration (sec) of the basis function. Note that this does not guarantee that the response will have fully decayed away within this many seconds, only that it will not be evaluated at longer times. Remember to always visually inspect your basis function, to ensure that it has the properties you expect!

  We recommend that you take the opportunity to try out multiple sets of parameter values and compare the plots of the resulting HRFs. And that you likewise explore the impact of modifying parameter values for any other type of basis function that you may wish to use. The basis functions corresponding to the other menu options are shown in Figures 6-13 through 6-17. In some instances a plot contains more than one curve. In these cases, nirsLAB will separately convolve each of the plotted functions with the experimental design models that you will specify in the next step.

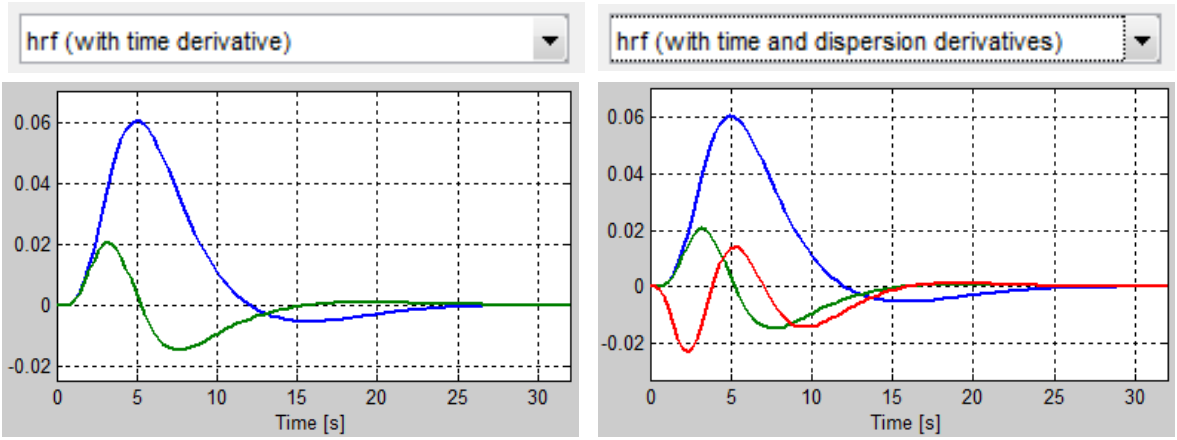

Figure 6-13. Basis-function plots for the two augmented versions of the canonical hemodynamic response functions. The theoretical rationale for adding the derivative terms is that this extends the range of physiological times-to-peak, peak-width, *etc*., that are well modeled by the particular set of parameter values chosen.

Figure 6-14. (Top) Detail view of the changes, produced by selecting 'Fourier set' in the drop-down menu, to the 'Specify basis function:' row of the 'Model Specification' module of the *Parameter Setup for GLM Analysis (Level 1)* GUI (Figure 6-10). The theoretical rationale for this type of basis function is that it can accurately approximate a physiological hemodynamic response of arbitrary shape. (Bottom left) Plot of the default Fourier basis set. The first parameter value is the largest number (default value = 4) of complete sinusoid periods in the set. Thus there are 9 functions altogether: sine and cosine wave of 1-4 complete cycles, plus a constant. (Bottom right) Plot of the Fourier basis set obtained when the first parameter value is changed to 1.

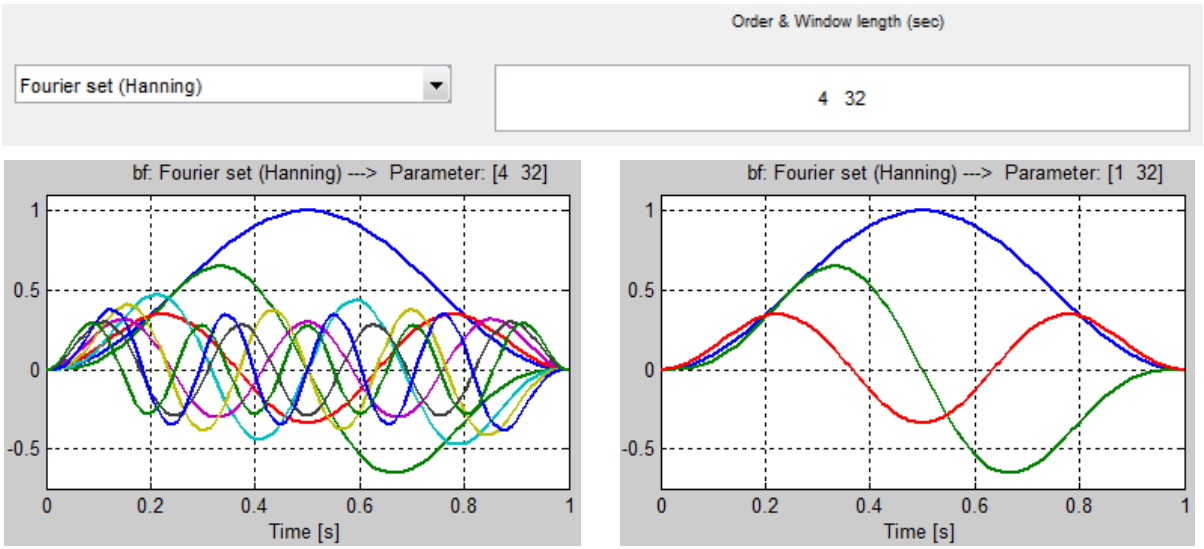
Order & Window length (sec)
Fourier set (Hanning)
4 32
bf: Fourier set (Hanning) ---> Parameter: [4 32]
bf: Fourier set (Hanning) ---> Parameter: [1 32]
Time [s]
Time [s]

Figure 6-15. Counterpart to the information shown in Figure 6-14, when the 'Fourier set (Hanning)' menu item is selected. The functions in the basis set are the same (*i.e.*, sinusoids and constants) as for the 'Fourier set' basis, with the added property that each of them is multiplied by a "Hanning window function".

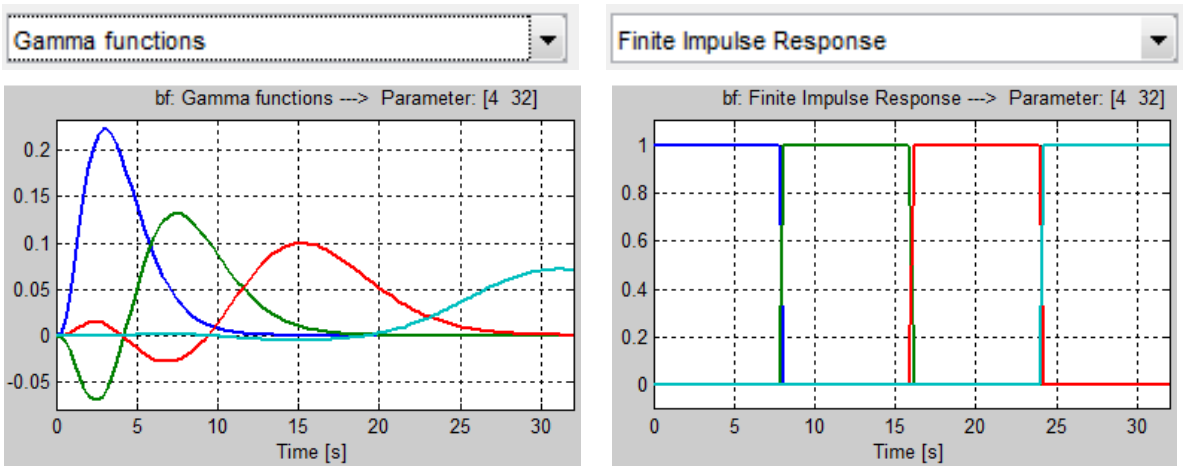
Gamma functions
bf: Gamma functions ---> Parameter: [4 32]
Time [s]
Finite Impulse Response
bf: Finite Impulse Response ---> Parameter: [4 32]
Time [s]

Figure 6-16. Basis-function plots for the 'Gamma functions' and 'Finite Impulse Response' drop-down menu items. As with the 'Fourier set' (Figure 6-14), the theoretical rationale for these types of basis function is that they can accurately approximate physiological henodynamic responses of arbitrary shape. The first parameter (default value = 4) is the number of functions in the set, and the second (default value = 32) is the time interval (in seconds) over which they are computed.

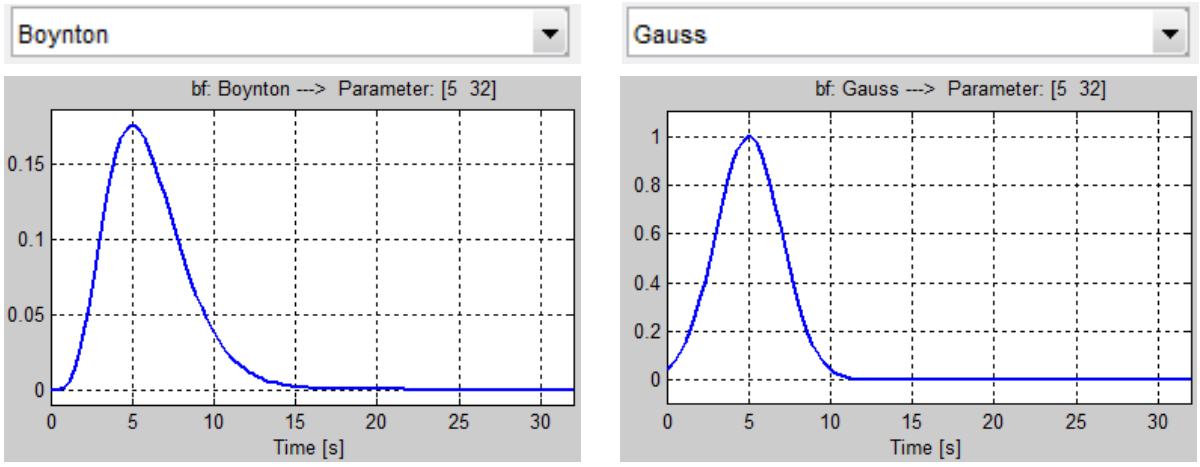

Figure 6-17. Basis-function plots for the 'Boynton' and 'Gauss' drop-down menu items. These are qualitatively similar to the canonical hemodynamic response function, but have fewer parameters. The first parameter (default value = 5) is the time-to-peak (in seconds), and the second (default value = 32) is the time interval (sec) over which they are computed. Note that the width of the peak cannot be independently specified, but is fully determined once you specify a value for the time-to-peak parameter.

'Specify (multiple) conditions:'. The information supplied to nirsLAB in this model specification step is used to generate a project-specific design matrix for GLM. The design matrix has the same number of rows as the number of data time frames in the dataset, and a number of columns equal to the number of different patterns of hemodynamic variation that you expect to find in the detector data. A simple demonstrational example of a design matrix is:

$$\mathbf{X} = \begin{bmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 \\ 0 & 0 & 0 & 1 \\ 0 & 1 & 1 & 1 \\ 0 & 1 & 0 & 1 \\ 1 & 0 & 1 & 1 \\ 1 & 0 & 0 & 1 \\ 1 & 1 & 1 & 1 \\ 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 1 \end{bmatrix},$$

where the alternating 1s and 0s in the first three columns indicate the time frames when an experimental condition (*e.g.*, a sensory stimulus, motor task, or cognitive challenge) was present (1 = "on") or absent (0 = "off"). Models of this type are commonly referred to as "boxcar functions." Note, however, that experimental-condition models are not required to be periodic, or to have "on" and "off" periods of equal duration, or to have only two states. For example, if a task has more than one difficulty level, the corresponding column of the design matrix might use values of 0, 1, 2, ... to denote the different levels (0 = "off," 1 = "easy," 2 = "more difficult," ...). Alternatively, the design matrix could have a distinct column for each task level, each having the sort of binary off/on structure as depicted above.

The fourth, constant-value column in the preceding design-matrix example is analogous to the intercept in the general formula for a straight line. Its purpose is to account for the non-zero time-average value that may be present in the each channel's data. In contrast to the experimental-protocol models, this model accounts for a phenomenon that likely is present in the data (*i.e.*, different mean values in different channels) but probably will not be of interest to you. It is included in the design matrix in order to "soak up" a percentage of the data variance that, if not accounted for in this way, could negatively impact your ability to see the true effects of the experimental-design conditions.

As shown in Figure 6-18, there are two items in the 'Specify (multiple) conditions:' drop-down menu. (In contrast to the 'Specify basis function:' menu, here the 'none' option is not a valid choice. We made 'none' the default in order to ensure that you will make a deliberate selection and will not inadvertently skip this step.)

- If you choose the 'nirsLAB condition file' menu item, the design matrix is constructed from information in the files that nirsLAB previously saved in the *Conditions* sub-folder described in Chap. 2, Section 4.3. That is to say, a design-matrix column will be generated for each experimental condition that you either created or loaded in the *Set markers* GUI (Chap. 2, Section 4), and the event onsets and durations information that

you specified determines which entries in each column have the value '1' and which are '0'.

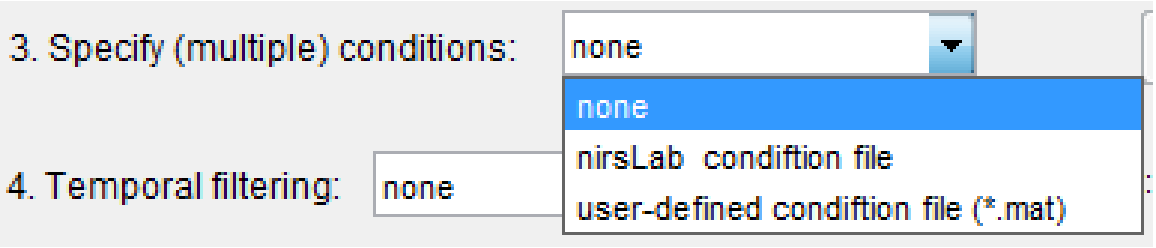

Figure 6-18. Detail view of the 'Specify (multiple) conditions' drop-down menu in the 'Model Specification' module of the *Parameter Setup for GLM Analysis (Level 1)* GUI (Figure 6-10).

- The 'user-defined condition file (*.mat) menu item will allow you to read in model-function information from any file that you may have stored it in (using the appropriate file format), even if that file is not yet associated with the project. However, the relevant segment of the nirsLAB source code is under development at this time, so selecting this option will produce the pop-up message asking you to use the 'nirsLAB condition file' option instead.

After you make your selection, the *View Convolution Model(s)* button, initially grayed out as shown in Figure 6-10, will be enabled (Figure 6-19). Clicking on that button will cause two graphics windows like the ones in Figure 6-19 to pop open. (These were generated using the oxygenated hemoglobin time series from the demo1 data set, and the 'hrf' basis function.) The red curve that appears in both (because there are two experimental conditions)

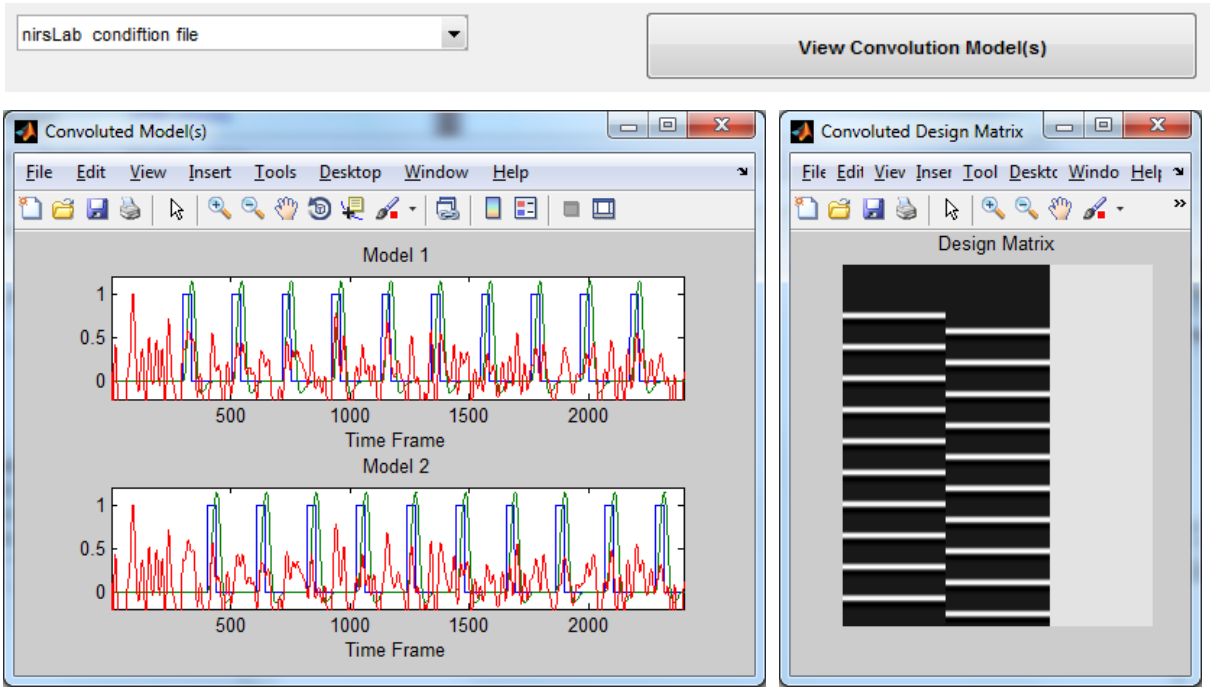

Figure 6-19. (Top) Detail view of changes in the 'Specify (multiple) condition:' line when the 'nirsLAB condition file' menu item is selected. (Bottom) Clicking on the now-enabled *View Convolution Model(s)* button generates the *Convoluted Model(s)* (left) and *Convoluted Design Matrix* (right) graphics windows.

sub-plots of the *Convoluted Model(s)* window is the hemodynamic-state time series, averaged over all channels included in the probeInfo file and rescaled so it can be plotted on the same axes as the other model-function information. The blue and green curves show the model-function values extracted from the conditions file, both before (blue) and after (green) the onsets-and-durations information is convolved with the basis function. The post-convolution curves exhibit the properties that we expect to find in hemodynamic-response data: the onset and cessation of finger tapping should lead to more gradual changes in the hemodynamic state. This corresponds to continuously varying values in the design-matrix columns, rather than instantaneous shifts from 0 to 1 and back. The *Convoluted Design Matrix* window shows you a graphical representation of the post-convolution design matrix, including the constant term. Each gray level here corresponds to a different y-axis value for the green curves in the *Convoluted Model(s)* window.

'Temporal filtering:'. In some cases, the constant-value design matrix column will not be sufficient for the purpose of "soaking up" the portion of the data variance that is not related to the experimental conditions and can negatively impact your ability to see the true effects of those conditions on the hemodynamic states. To generate additional design-matrix columns to account for data variance unrelated to the experimental design, select 'DCT' (**d**iscrete **c**osine **t**ransform) from the 'Temporal filtering:' drop-down menu (Figure 6-20). This will enable the adjacent 'Highpass frequency cutoff (s):' text field and the *View DCT Set* button.

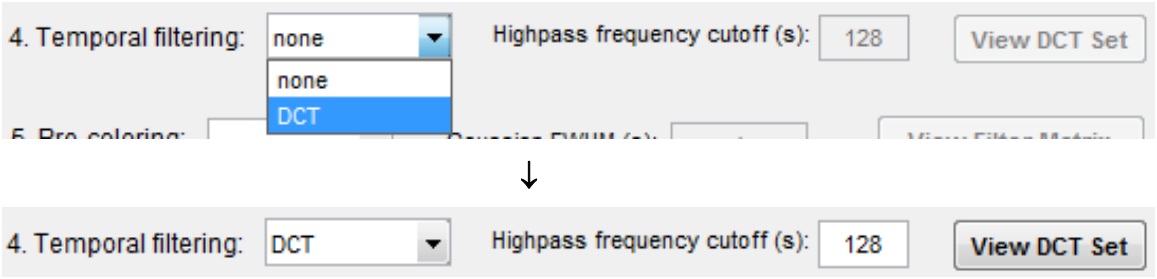

Figure 6-20. Detail view of changes in the 'Temporal filtering:' line of the 'Model Specification' module of the *Parameter Setup for GLM Analysis (Level 1)* GUI (Figure 6-10). Selecting 'DCT' from the drop-down menu enables the *View DCT Set* button, and clicking on the button generates the graphics windows shown in Figure 6-21.

Click on the button to launch the two *DCT set* windows shown in Figure 6-21. The curves shown in these figures (overlaid colored x-y plots in the first, separated gray-scale surface map in the second) are additional design-matrix columns that define sinusoidal rhythms having different frequencies. The significance of the number in the 'Highpass frequency cutoff (s):' field is that fluctuations with periods longer than that number of seconds will be suppressed (*i.e.*, partially accounted for by the sinusoidal models), while shorter-period fluctuations will be regarded as part of the signal you are trying to account for with the experimental-condition models. You may

enter a number greater than the 128-seconds (*i.e.*, the cutoff frequency is 1/128 s^{-1} ≈ 0.008 Hz) default value if you want the signal suppression to end at longer-period fluctuations (*i.e.*, a lower frequency, to ensure that the DCT frequency band does not overlap with any event-related frequencies). Click on the *View DCT Set* button again to view the result, as in the example shown in Figure 6-22. You may also enter a number smaller than 128 if you want to suppress shorter-period (higher frequency) signals than the 128 s (0.008 Hz) default.

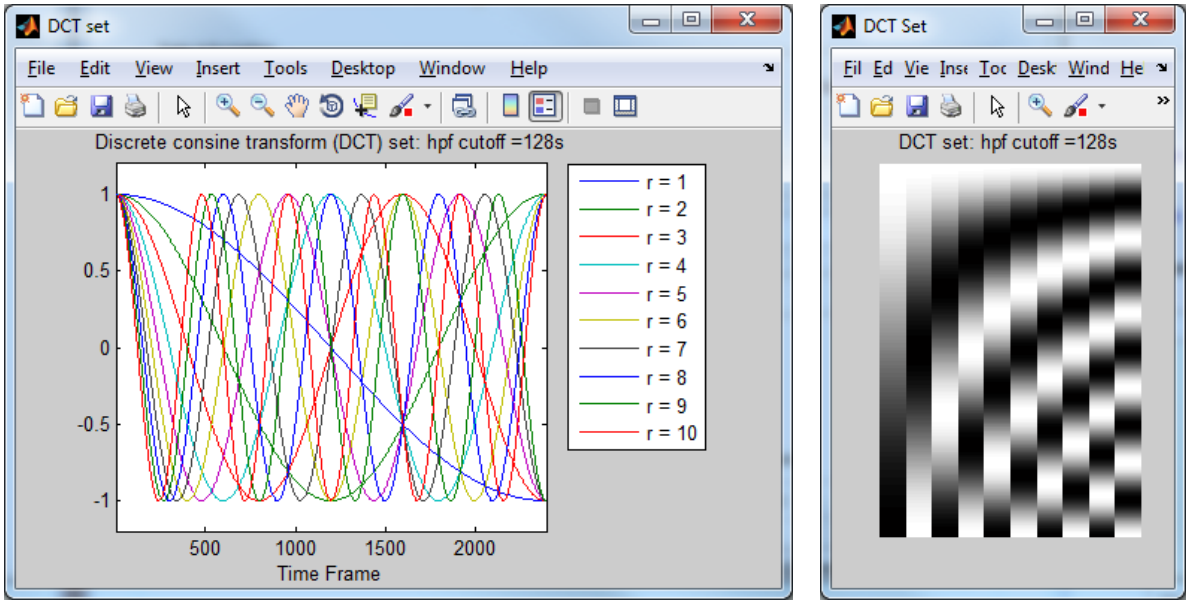

Figure 6-21. Graphics windows that pop open when the *View DCT Set* button (Figure 6-20) is clicked. The additional design-matrix columns are plotted in both, in the same two formats as used for displaying the event-related models (Figure 6-19).

Note that the graphics windows depicted in Figures 6-21 and 6-22 will not automatically close, but must be closed manually.

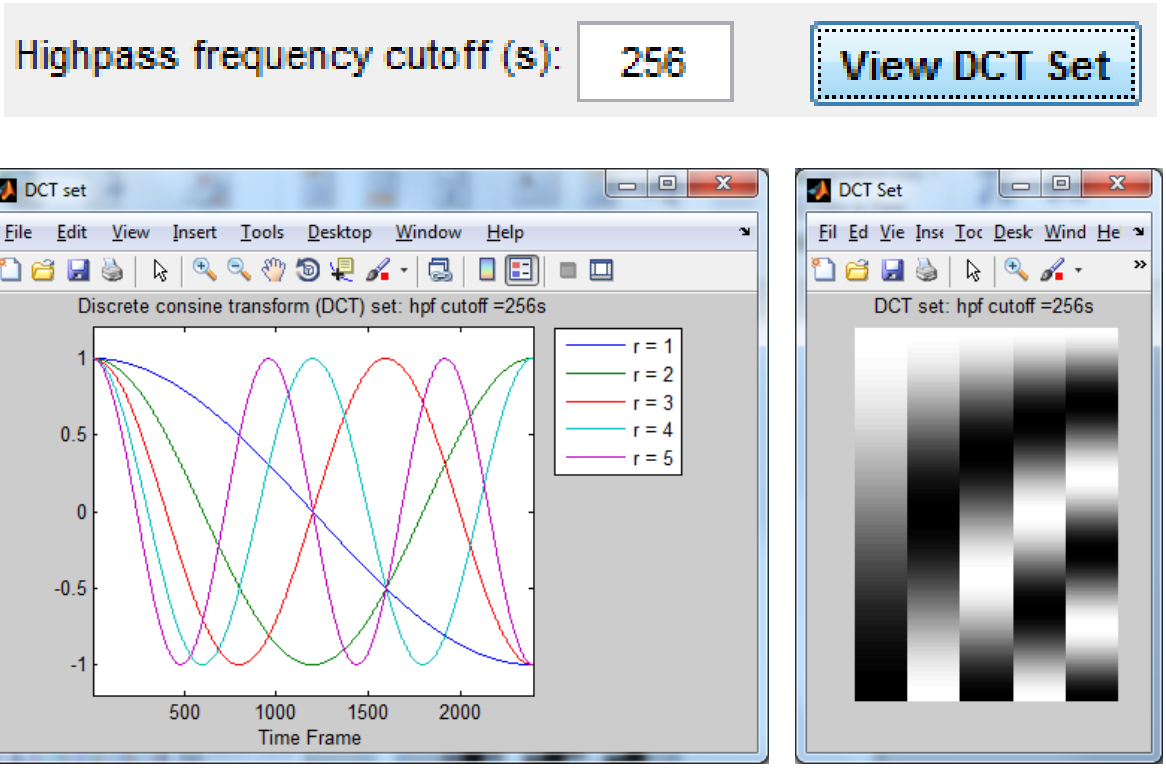

Figure 6-22. The effect of changing the numerical value in the 'Highpass frequency cutoff (s):' field. Comparing this result to the one in Figure 6-21, we see that the number of models in the DCT set is inversely proportional to the specified cutoff.

'Pre-coloring:'. In order to maximize the accuracy of the statistical inferences that you will draw from the GLM computations, it is important for you to account for the fact that the value of a hemodynamic state's noise component (for more on what this is, see Section 2.2.2) at one time frame is correlated with the values it has at the frames immediately preceding and following it, and that the correlation falls off as the lag between two time frames increases. This phenomenon is called "serial correlation." One of the strategies that have been developed for dealing with serially correlated noise is known as pre-coloring, which means that the GLM formulation includes a mathematical term that explicitly models the dependence of the correlation on the time interval between two data values. Unfortunately, the exact nature of that dependence is not going to be the same for any two fNIRS data sets, and it is difficult to experimentally evaluate it for any one of them. A way around this is to mathematically pre-treat the hemodynamic-state time series in a manner that imposes a known noise correlation structure on it (without significantly distorting the event-related information of interest in the process).

To apply pre-coloring, select either the 'Gaussian' or the 'hrf' option from the 'Pre-coloring:' drop-down menu, as illustrated in Figures 6-23 and 6-24. If you select 'Gaussian', you will have the option of specifying a FWHM (**f**ull-**w**idth at **h**alf-**m**aximum; for a Gaussian, 1 FWHM ≈ 2.4

standard deviations) that is different from the 4-second default value (*e.g.*, if you have experiment-based estimates of the duration of the serial correlation in your data time series).

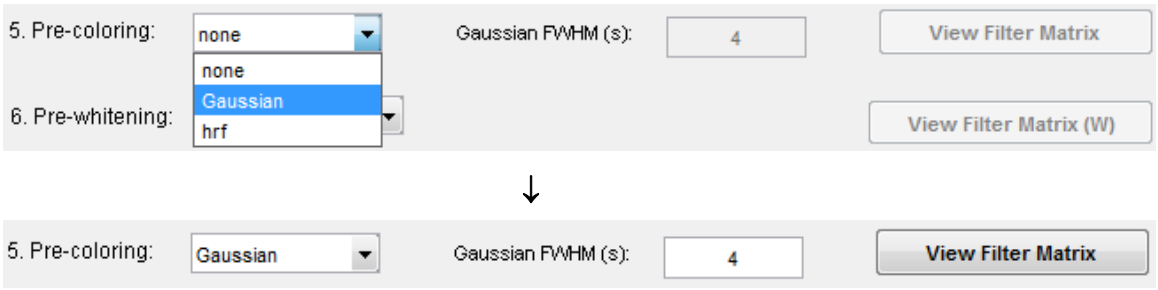

Figure 6-23. Selecting the 'Gaussian' option from the 'Pre-coloring:' drop-down menu enables the 'Gaussian FWHM (s):' field and *View Filter Matrix* button. If you have reason to, you may change the default 4-second FWHM (~1.7-second standard deviation) to either a larger or a smaller value.

If you select 'hrf', then the GLM computation will proceed under the assumption that the noise-component serial correlation is proportional to the value of your previously specified basis function, adjusted so that the maximum correlation occurs when the time lag is zero (since every noise-component value is perfectly correlated with itself).

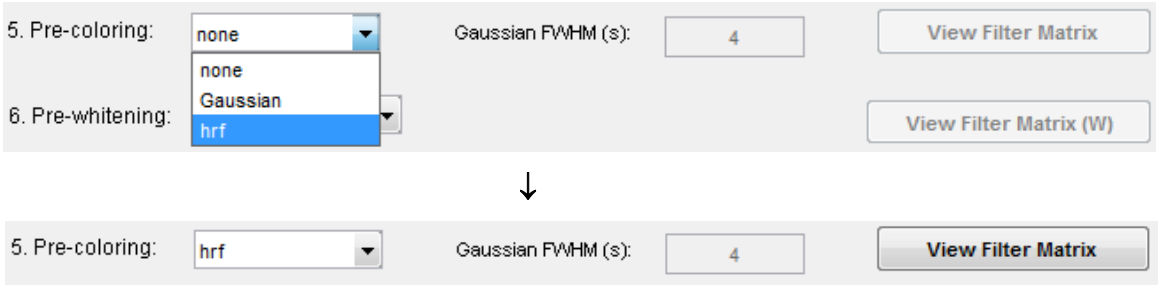

Figure 6-24. Selecting the 'hrf' option from the 'Pre-coloring:' drop-down menu enables the *View Filter Matrix* button. Here the width of the pre-coloring function is determined by the basis function specified in a previous step. The only way to modify it is to specify a different basis function.

Click on the *View Filter Matrix* button to open a window in which the serial correlation matrix is displayed as a color-scale map, as shown in Figure 6-25. (Refinements such as a color axis and a logarithmic scaling option will be offered in future releases of nirsLAB.)

The pre-coloring operation involves convolving the hemodynamic-state time series with the selected function. The resulting modified time series will have a noise correlation structure close to that for a Gaussian distribution or to the basis function, and these correlation structures are well-characterized.

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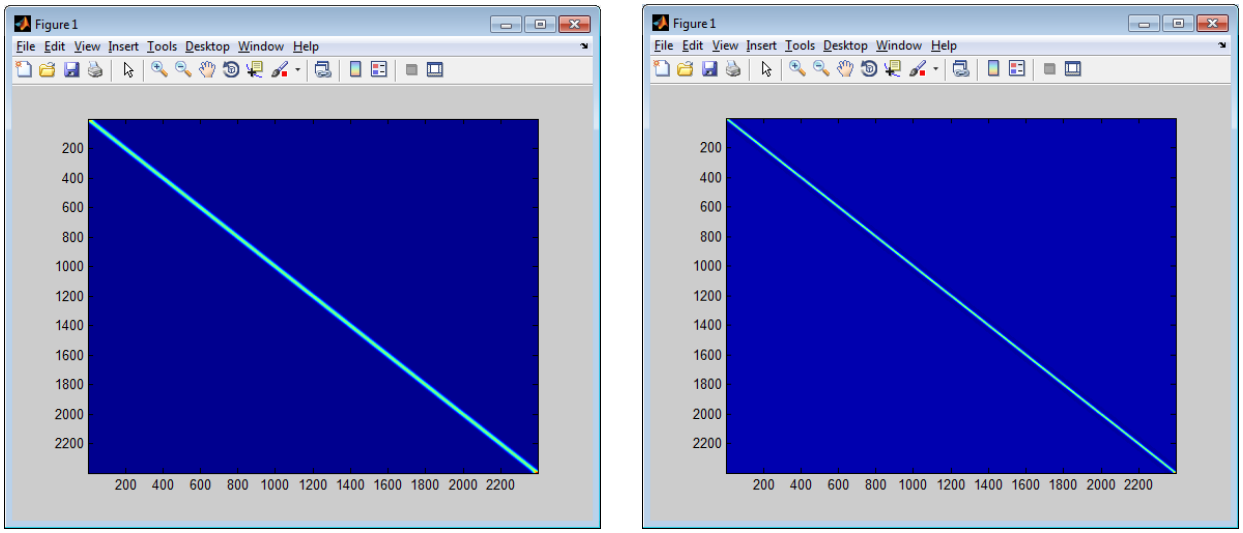


Figure 1
File Edit View Insert Tools Desktop Window Help
200 400 600 800 1000 1200 1400 1600 1800 2000 2200
Figure 1
File Edit View Insert Tools Desktop Window Help
200 400 600 800 1000 1200 1400 1600 1800 2000 2200

Figure 6-25. Clicking on the *View Filter Matrix* button produces a graphical representation of the pre-coloring function in a pop-up window. (Left) 'Gaussian' result, with the default 4-s FWHM. (Right) 'hrf' result, for the canonical HRF basis function with default parameter values.

'Pre-whitening:'. Another strategy for handling time series that have (or at least might have) serially correlated noise is known as pre-whitening. This means that the data are mathematically pre-treated with an algorithm that attempts to remove the influence of the noise value at any instant on the noise values at later times (again, without distorting the event-related information of interest in the process).

To apply pre-whitening, select 'AR(1)' (**a**uto**r**egression of order **1**; this is the only option available at this time) from the 'Pre-whitening:' drop-down menu (Figure 6-26).

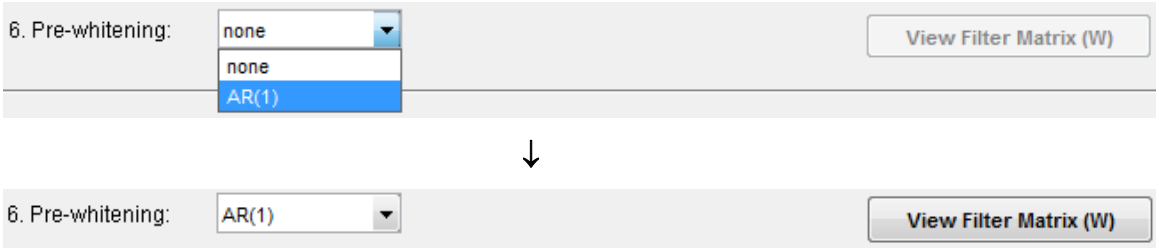


Figure 6-26. Selecting the 'AR(1)' item from the 'Pre-coloring:' drop-down menu enables the *View Filter Matrix (W)* button.

For every hemodynamic-state time series in your dataset, the AR(1) algorithm fits the data to a model of the form $x(t_i)=a+b\cdot x(t_{i-1})$, and it finds those values for the coefficients *a* and *b* that minimize the difference between $x(t_i)$ and $a+b\cdot x(t_{i-1})$. The GLM computation subsequently operates upon the residual, $r(t_i)=x(t_i)-a-b\cdot x(t_{i-1})$, which has substantially less serial correlation than the original data. Click on the *View Filter Matrix (W)* button to open a window

that displays a color-scale map showing which data values are used as predictors for each subsequent one, as in Figure 6-27. (Note that, since only order-1 autoregression is used at present, what is seen is a simple identity matrix.)

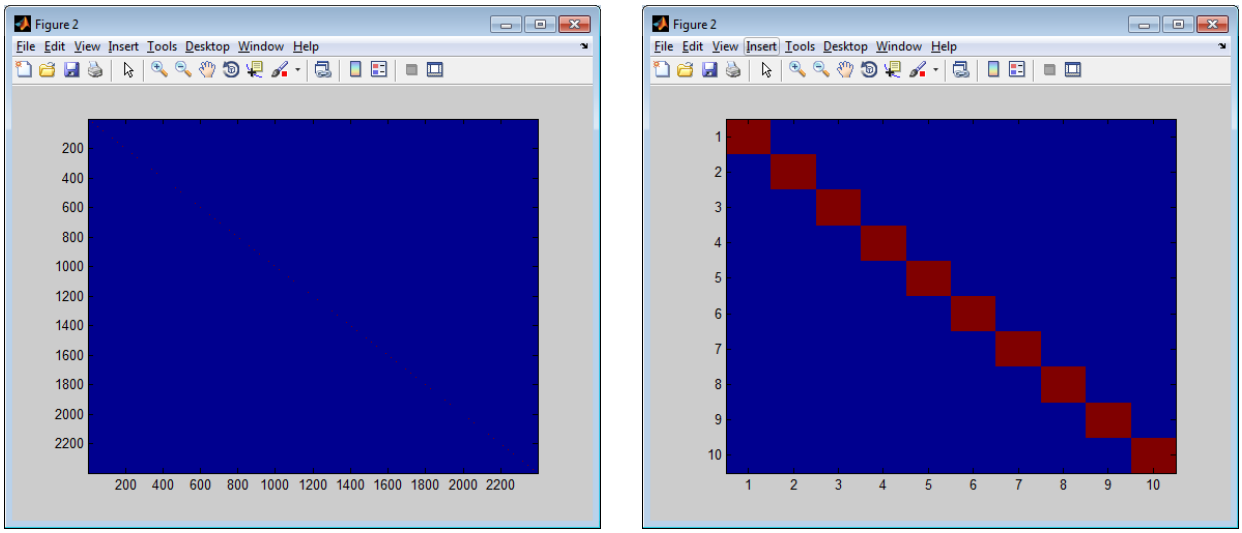


Figure 6-27. Clicking on the *View Filter Matrix (W)* button produces a graphical representation of the pre-whitening function (which is an identity matrix in the case of AR(1)) in a pop-up window. (Left) The full matrix, where the non-zero values are difficult to see because they lie only on the main diagonal. (Right) Enlarged view of a small portion of the same matrix, revealing the non-zero diagonal values.

Click on the *Confirm Model specification* button at the top of the 'Model Specification' module (Figure 6-10), to generate a design matrix incorporating the experimental conditions, basis function(s), and more advanced options that you have specified. During this process a graphics pop-up window will open (Figure 6-28), showing a gray-scale map of the columns of the design matrix that are related to experimental conditions (and also the constant term, but not the DCT terms that you may have specified). The *Parameter Setup for GLM Analysis (Level 1)* GUI will close automatically. You can also terminate the GUI without confirming your parameter specification, by clicking on the *Close* button.

2.2.2 Estimating GLM coefficients

In the 'GLM analysis' module (Figure 6-9) of the *Statistical Parametric Mapping Level 1 (within subject)* GUI (Figure 6-2), click on the *Estimate GLM coefficients* button to start the process of solving the GLM equation, $\mathbf{Y} = \mathbf{X\beta} + \mathbf{E}$. The variables in the equation are:

- **Y** is the matrix of hemodynamic data. Its dimensions are $N_t \times N_s$, where N_t is the number of measurement time frames and N_s is the number of channels.
- **X** is the design matrix, whose generation is described in Section 2.2.1. Its dimensions are $N_t \times N_m$, where N_m is the total number of models (including the constant and any terms that you may have included to account for sources of variance not related to the experimental design).

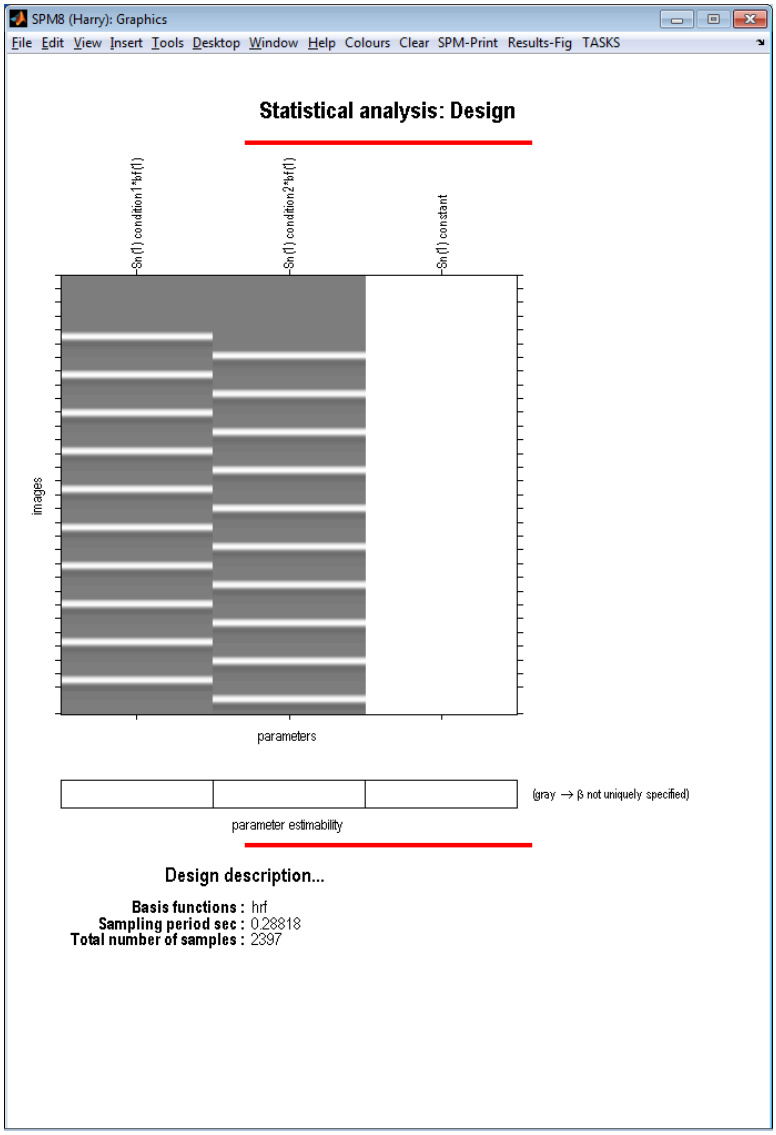


Figure 6-28. Example of the final GLM design matrix display, which is generated when you click on the *Confirm Model specification* button (Figure 6-10).

- **β** is a $N_m \times N_s$ matrix of numbers that, when multiplied by **X**, produces linear combinations of design-matrix columns that are the maximally accurate approximations to the hemodynamic time series. This matrix is the unknown quantity that is solved for in the GLM computation; hence it is referred to as the "GLM-parameter matrix" or "GLM-coefficient matrix."

- **E** is the "error term" or "residual term." It has the same dimensions as **Y** and is the quantity that the GLM algorithm seeks to minimize (*i.e.*, the more accurately **Xβ** approximates **Y**, the smaller **E** becomes). The **E** matrix also is useful for evaluating whether theoretical assumptions that underlie the GLM technique are violated: for example, ideally every column of **E** will have the same standard deviation, the

correlation between any two columns of **E** will be zero, and the elements of **E** will be normally distributed.

For estimation of β, nirsLAB uses a SPM-based algorithm called ReML (**re**stricted **m**aximum **l**ikelihood) to compute a least-squares solution to an overdetermined system of linear equations. Under ideal conditions the ReML solution is the same as the solution obtained with any other method for solving systems of linear equations. But ReML is more robust than other methods to non-ideal effects, such as the presence of uncontrolled sources of variance in the measurement data.

In practice, you should notice that the estimation process runs quickly if you used a pre-coloring option to correct for serial autocorrelation (or if you did not use either method). In contrast, if you used the pre-whitening option, then nirsLAB will resort to an iterative nonlinear optimization algorithm to solve the GLM equation. The optimization algorithm frequently converges *but convergence is not guaranteed*. If it fails to converge for the dataset you are analyzing, you will need to re-generate the conditions file using a different serial correlation correction.

When the GLM computation is complete, a 'Help dialog' pop-up will open, displaying the path and name of the output file.

2.3 'SPM result visualization' module

Click on the *View SPM results* button in the 'SPM result visualization' module of the *Statistical Parametric Mapping Level 1 (within subject)* GUI (Figure 6-2). This will launch the *SPM Result Viewer* GUI depicted in Figure 6-29. Note that the message shown in the *Specify SPM Result* field is displayed only if

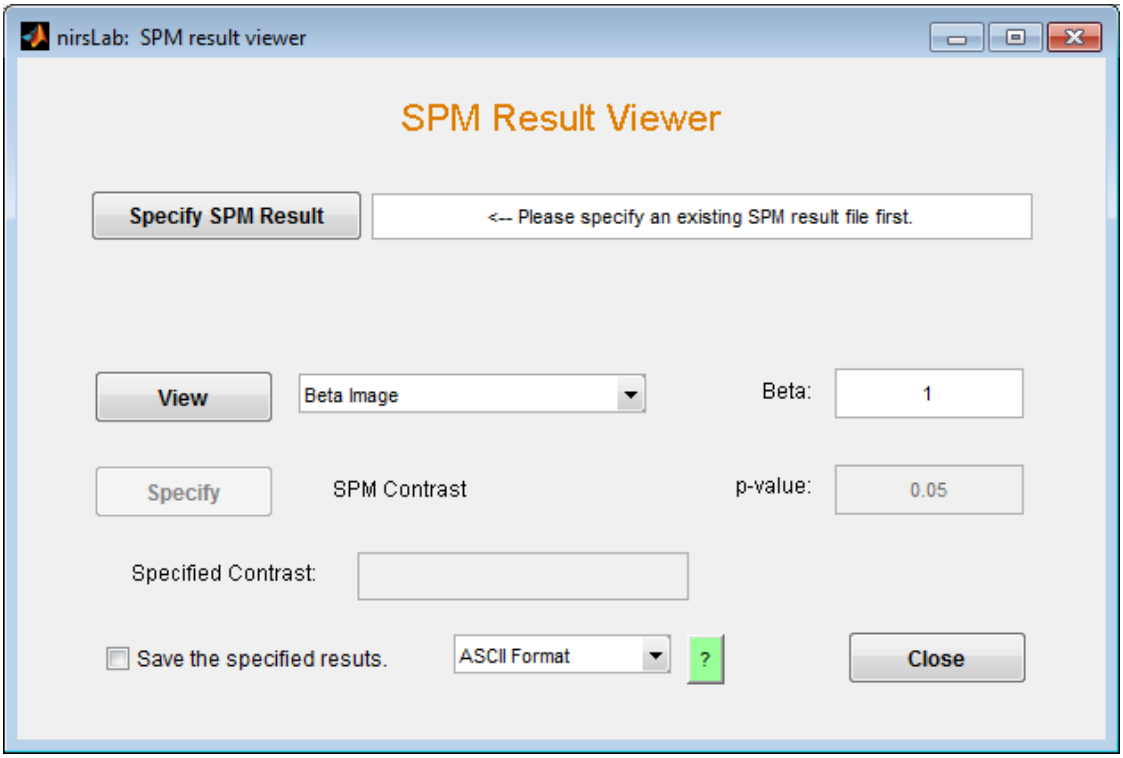


Figure 6-29. The *SPM Result Viewer* GUI.

You have not yet performed any Level-1 GLM computations during the current MATLAB session. If you have, then the same field will show the name and location of the most recently generated results file. In either case, you may select a (different) file to view. Clicking on the *Specify SPM Result* button shown in Figure 6-29 launches a browser window that you can use to navigate to and select the file you are interested in. When a file is selected, a new text line appears in the GUI, indicating the number of computed β values (*i.e.*, the number of models in the design matrix) for each channel. An example of this is shown in Figure 6-30.

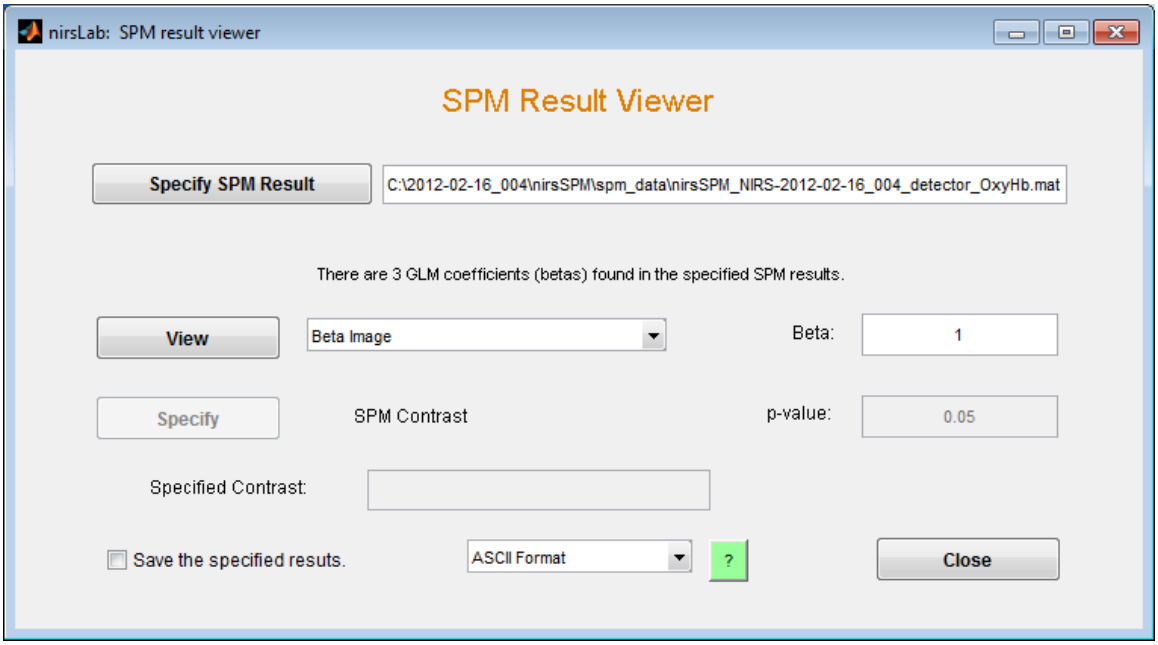


Figure 6-30. The *SPM Result Viewer* GUI after a Level-1 SPM output file has been specified.

From the drop-down menu next to the *View* button, select the GLM-related parameter that you want to view. The available menu selections, as shown in Figure 6-31, are:

- 'Beta Image': A "beta" (*i.e.*, Greek letter *β*) is one of the coefficients that the GLM model uses to explain fluctuations in the image data in terms of the temporal models in the design matrix. This is expressed mathematically as $y(t) = y(t) = \beta_1 \cdot x_1(t) + \beta_2 \cdot x_2(t) \ldots + \beta_M \cdot x_M(t)$, where $y(t)$ is the hemodynamic-state value for a given channel, and $x_1(t)$, $x_2(t)$, …, $x_M(t)$ are the models included in the design matrix. The ReML algorithm finds the specific values for β_1, β_2 … , β_M that make the two sides of the preceding equation as nearly equal as possible.

- 'Contrast Image': A contrast is a weighted sum of one or more models from the design matrix, embodying a biological hypothesis that you wish to evaluate. For example, suppose that the models $x_1(t)$ and $x_2(t)$ tell you when two different experimental tasks (*e.g.*, left-hand and right-hand finger tapping) were performed by the subject, and you want to know if the second induces a larger hemodynamic response than the first does. The resulting contrast image will show you the value of the difference $\beta_2 - \beta_1$, which is close to zero in channels where the two experimental conditions have comparable

effects, positive in channels where the second has a larger absolute effect that the first, and negative in channels where the first has a larger absolute effect than the second.

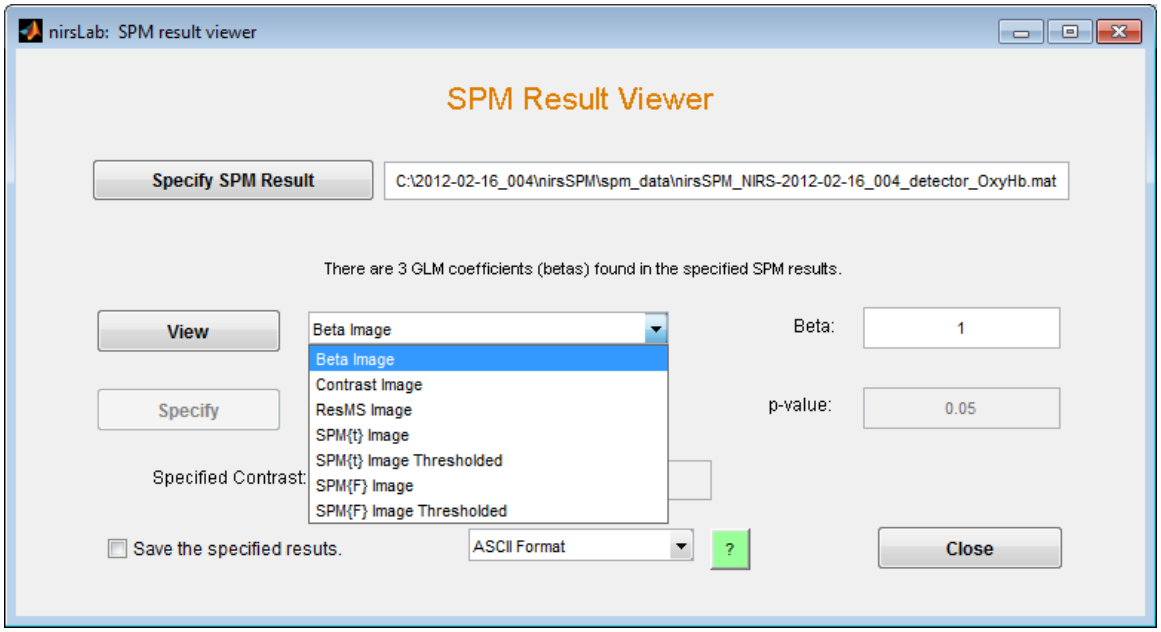


Figure 6-31. The *View* drop-down menu.

- 'ResMS Image': The term 'ResMS' is an abbreviation for "**res**idual **m**ean **s**quare"; in other words, a ResMS image shows you the spatial distribution of values in the **E** matrix described above. Inspection of this image, which ideally will show little if any spatial structure, can assist you in deciding how well your design matrix satisfies the theoretical assumptions underlying the GLM analysis.

- 'SPM{t} Image': Interpretation of beta and contrast values can be difficult, because they are determined by two distinct factors: 1) how closely the time-varying GLM models approximate the time-varying hemodynamic image values; 2) the magnitude or amplitude of the fluctuations in each channel. To allow for an unambiguous assessment, nirsLAB can compute a t-statistic that primarily considers the first of the preceding factors. The t-statistic is a normalized, dimensionless number. Let us continue to use the hypothetical example considered in the 'Contrast Image' item. Then the SPM{t} image has positive values in channels where the second experimental condition has a larger relative effect that the first, and is negative in channels where the first has a larger relative effect that the second.

- 'SPM{t} Image Thresholded': For the preceding menu option, the displayed image will show you the t-statistic values in all image channels. But the computed value of a t-statistic will rarely be exactly zero, even in channels where the hemodynamic effects of the two experimental conditions really do have the same amplitude. If you choose the 'SPM{t} Image Thesholded' option, the displayed image will have non-zero values in only the channels where the t-statistic is statistically significant and is positive-valued. (To see

which channels have statistically significant negative t-statistic values, it is necessary to specify another contrast that reverses the algebraic signs of the first contrast.)

- 'SPM{F} Image': Some biological hypotheses involve comparisons of three or more experimental conditions. For example, you may want to know if there are any differences among the hemodynamic responses elicited by three auditory stimuli, that is, whether or not β_1, β_2 and β_3 are all the same. Other hypotheses involve comparisons among two or more contrasts, for example, if $\beta_2 - \beta_1$ is different from $\beta_3 - \beta_2$. These types of comparisons can be performed by using the F-test capability of nirsLAB. The F-statistic is a dimensionless quantity that has large values if the experimental conditions induce different hemodynamic responses (which in turn give rise to different beta values or contrasts of beta values).
- 'SPM{F} Image Thresholded': If you choose the 'SPM{F} Image' option, the displayed image will show you the F-statistic values in all image channels. If you choose the 'SPM{F} Image Thesholded' option, the displayed image will have non-zero values in only the channels where the F-statistic is statistically significant.

To view a beta image (refer to Figures 6-30 and 6-31 as needed):

1. Select 'Beta Image' from the drop-down menu.
2. Enter a model number (*i.e.*, design-matrix column) in the 'Beta:' number field.
3. Click on the *View* button. The spatial distribution of the GLM coefficient you have selected will be displayed in a GUI whose default format is depicted in Figure 6-32. Note that its structure and display capabilities are very similar to those of the *MAP Hemodynamic states* GUI of the *Data Viewer* portal (Chap. 5). The hemodynamic state is not selected in the GUI, since the specified SPM output file contains results for only one state. And there isn't animation or scrolling capability, since there is no temporal dimension in GLM-computation results.

To view a contrast image (refer to Figures 6-30 and 6-31 as needed):

1. Select 'Contrast Image' from the drop-down menu. This will disable the 'Beta:' field and enable the *Specify SPM Contrast* button. Click on 'Specify SPM Contrast' to launch the *SPM contrast manager* GUI (Figure 6-33).
2. Click on the *Define new contrast...* button in the *SPM contrast manager* window. This will change the appearance of the *SPM contrast manager* GUI as indicated in Figure 6-33. In the '*name*' field, enter a name for the contrast you are going to define (*e.g.*, 'LmR', for "left minus right"). In the '*type*' field, select the 't-contrast' radio button.
3. We will consider the example described above: the models $x_1(t)$ and $x_2(t)$ correspond to the subject performing left- and right-hand finger tapping, and you want to know where each of task induces the larger hemodynamic response. Place the cursor in the '*contrast*' field and type "1 -1", then click on the *...submit* button, as demonstrated in Figure 6-34. (A value of 0 is automatically assigned to all models that follow the last one that you

explicitly assigned a value to. However, if there were more than two experimental-condition models and you were interested in the difference between the first and third ones, you would type "-1 0 1" in the '*contrast*' field.)

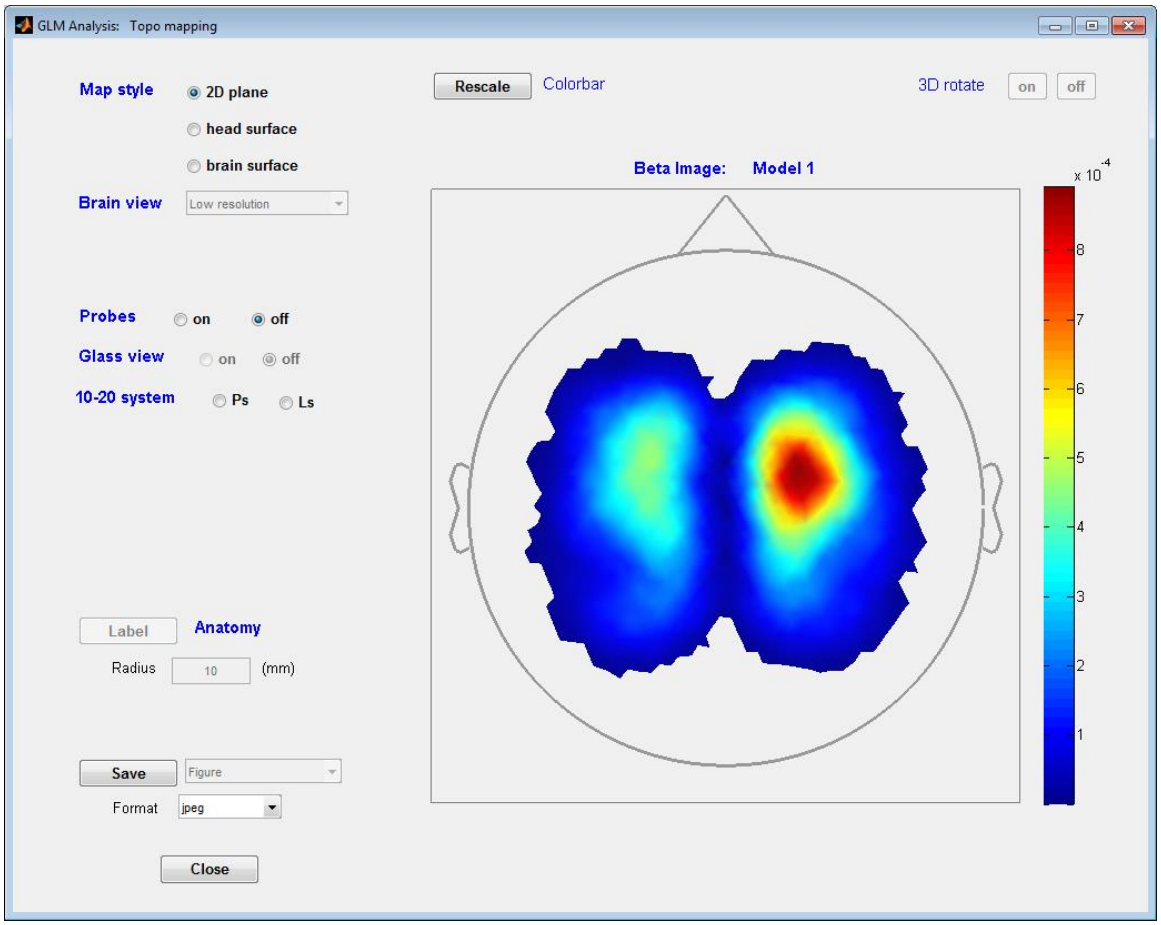


Figure 6-32. Example of a beta image display, with default viewer settings. The colors denote the magnitude of oxygenated hemoglobin response to left-hand finger tapping. As expected, the channels over the right side of the brain show larger responses than their counterparts on the left, while on both sides the greatest response in channels near the motor cortex.

4. Examine the graphical display of the contrast you have defined, in the right-hand side of the *SPM contrast manager* window, to ensure that it is what you intended. When you are satisfied, click on the *OK* button near the bottom of the window. Then click on the *Done* button near the bottom of the *SPM contrast manager* window.
5. Click on the *View* button. Proceed as in the 'Beta Image' case.

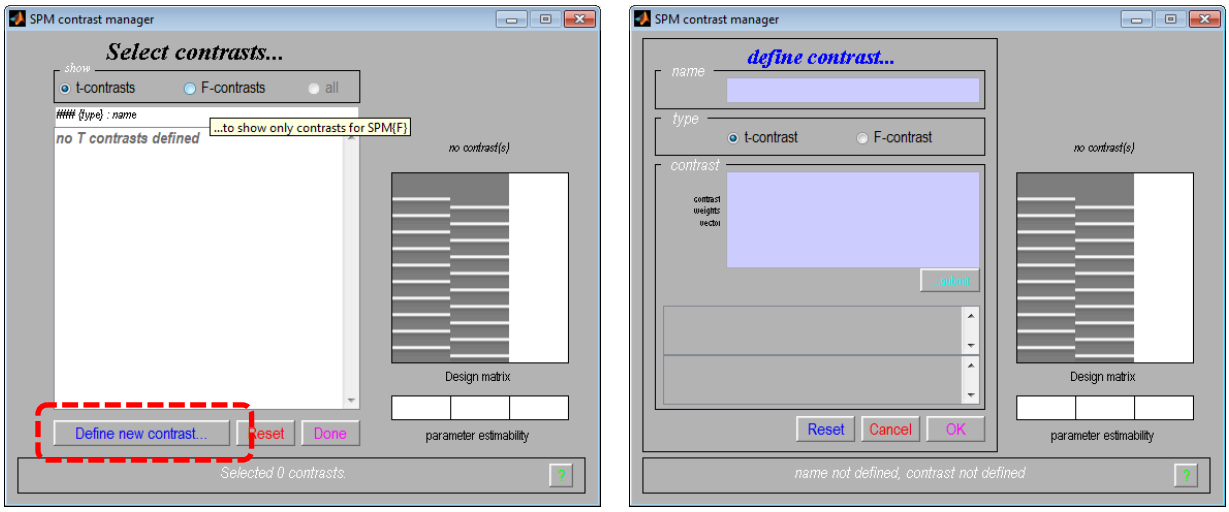


Figure 6-33. The *SPM contrast manager* GUI, before (left) and after (right) you click on the *Define new contrast…* button (red oval).

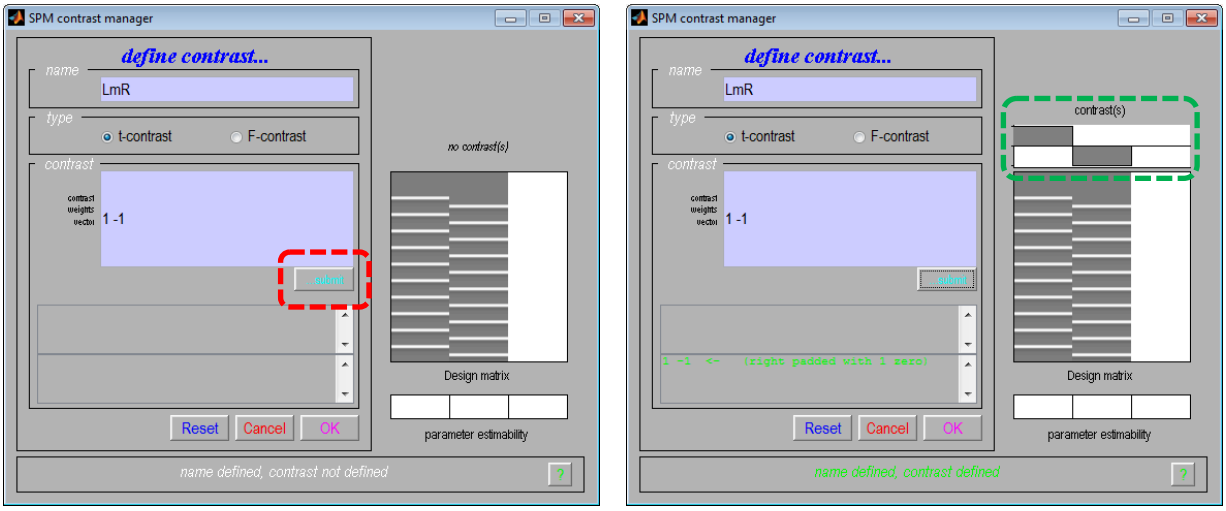


Figure 6-34. The *SPM contrast manager* GUI, after making entries in the '*name*' and '*contrast*' fields and before (left) and after (right) you click on the *…submit* button (red oval). The defined contrast is graphically depicted (green oval) above the design matrix.

To view a ResMS image (refer to Figure 6-31 as needed)

1. Select 'ResMS Image' from the drop-down menu.
2. Click on the *View* button, and proceed as in the 'Beta Image' case.

To view a SPM{t} image (refer to Figure 6-31 as needed):

1. Select 'SPM{t} Image' from the drop-down menu. This will enable the *Specify SPM Contrast* button.
2. Click on the *Specify SPM Contrast* button to launch the *SPM contrast manager* GUI.
3. Proceed as in the 'Contrast Image' case.

a. If you want to generate a t-statistic map for a single model, you can enter a single "1" in the '*contrast*' field. Enter "1" to get a t-statistic map for the first model, "0 1" for the second model, "0 0 1" for the third, *etc*.

To view a thresholded SPM{t} image (refer to Figures 6-30 and 6-31 as needed):

1. Select 'SPM{t} Image Thresholded' from the drop-down menu. This will enable the *Specify SPM Contrast button* and the 'p-value:' text field.
2. Enter a statistical significance level in the 'p-value' field. For example, if you enter "0.05," the resulting plot will show you the t-statistic values in all channels where the contrast is statistically significant at the $p<0.05$ level [one-side t-test (*i.e.*, only channels that have significant positive t-statistic values will be included), not corrected for multiple tests]. In all other channels, the original t-statistic values will be changed to zero.
3. Click on the *Specify SPM Contrast* button to launch the *SPM contrast manager* GUI.
4. Proceed as in the 'Contrast Image' case.
    a. To change the p-value threshold, simply enter the new value in the 'p-value' field and click on the *View* button. It is not necessary to repeat the contrast specification process.

To view a SPM{F} image (refer to Figure 6-31 as needed):

1. Select 'SPM{F} Image' from the drop-down menu. This will enable the *Specify SPM Contrast* button.
2. Click on the *Specify SPM Contrast* button to launch the *SPM contrast manager* GUI (Figure 6-33).
3. Click on the *Define new contrast...* button in the *SPM contrast manager* window. This will change the appearance of the GUI as indicated in Figure 6-33. In the '*name*' field, enter a name for the contrast you are going to define. In the '*type*' field, select the 'F-contrast' radio button.
    a. If you are not already familiar with the utility of F-contrasts, consider the hypothetical example of three distinct visual stimuli: there may be a difference between the hemodynamic responses associated with the first and second, and there may be a difference between the hemodynamic responses associated with the first and third, and you want to know whether there is a significant difference between the differences anywhere in the brain. To test for a higher-order relationship such as this, you would place the cursor in the '*contrast*' field and type either "1 -1 [Enter key] -1 0 1" or "1 -1 0 0; -1 0 1 0". Then, you would click on the *...submit* button.
4. Examine the graphical display of the contrast you have defined, in the right-hand side of the *SPM contrast manager* window, to ensure that it is what you intended. When you

are satisfied, click on the *OK* button near the bottom of the window. Then click on the *Done* button near the bottom of the SPM contrast manager window.

5. Click on the *View* button. Proceed as in the 'Beta Image' case.

To view a thresholded SPM{F} image:

1. Select 'SPM{F} Image Thresholded' from the drop-down menu. This will enable the *Specify SPM Contrast* button and the 'p-value:' text field.
2. Enter a statistical significance level in the 'p-value' field. For example, if you were to enter "1e-12," the resulting plot would show you the F-statistic values in all channels where the contrast is statistically significant at the p<1e-12 level (not corrected for multiple tests). In all other channels, the original F-statistic values will be changed to zero.
3. Click on the *Specify SPM Contrast* button to launch the *SPM contrast manager* GUI.
4. Proceed as in the 'SPM{F} Image' case.
    a. If you specify a contrast matrix containing only one row, then the resulting F-test will be equivalent to a two-sided t-test performed on the same contrast. The reason is that in this special case, the F-statistic value for any channel is the square of the t-statistic value for that same channel. That is, F-statistic values are always non-negative, whereas t-statistics may be either positive or negative. Thus the thresholded SPM{F} will have non-zero values in all channels where the F-statistic is statistically significant, whether the contrast value is positive or negative.
    b. To change the p-value threshold, simply enter the new value in the 'p-value' field and click on the *View* button. It is not necessary to repeat the contrast specification process.

To save the values for any of the *View* menu items in a file, choose a preferred format (ASCII or a MATLAB structure array) from the drop-down menu at the bottom of the *SPM Result Viewer* GUI. Then click in the 'Save the specified results.' checkbox near the lower left corner of the GUI. This instructs nirsLAB to create a sub-folder (unless it already exists), named either 'ASCII' or 'MAT', in the folder from which you loaded the Level-1 SPM output file (recall that by default, Level-1 results are saved in folders named 'spm_data'). The GLM-related quantity that you have selected from the *View* menu will be saved in the 'ASCII' or 'MAT' sub-folder. It will be saved as either a simple rectangular array of numbers (ASCII format), where the columns correspond to the channels in the same order they were specified in when the probeInfo file was generated (Chap. 7), or as a two-field structure array (MATLAB format). In the latter case, the 'data' field contains the same rectangular array as in the ASCII-format case, and the 'params' field contains other relevant information such as the data type (*i.e.*, which menu item was selected), and the contrast definition (if the data type is 'Contrast' or either thresholded or un-thresholded 'SPM{t}' or SPM{F}).

3 SPM Level 2

The following steps are carried out using the functions and utilities in the *Statistical Parametric Mapping Level 2 (between-subjects)* GUI (Figure 6-2).

1. Specify and load multiple SPM Level-1 data sets.
   - In the 'Multiple Data Specification' module (Figure 6-35), enter the number of distinct subject groups in the 'Number of groups:' field, and the numbers of subjects in each group in the 'Number of subjects:' field.

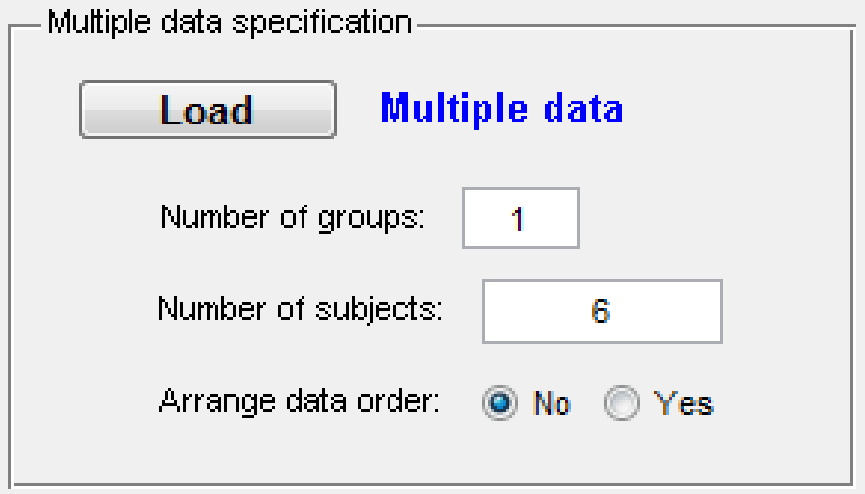


Figure 6-35. Detail view of the 'Multiple Data Specification' module of the *Statistical Parametric Mapping Level 2 (between-subjects)* GUI. While the default number of groups is two, with five subjects in each one (Figure 6-2), the set of Level-1 SPM output files that we have assembled for purposes of demonstration constitute a single six-subject group.

- Press the *Load Multiple data* button to launch a a browser window that you can use to navigate to and select a file containing previously generated Level-1 results, for each subject in turn (Figure 6-36).
  - So that you won't lose your place during the process of loading multiple datasets, the title bar initially reads 'Specify Group1 Subject**1** nirsLAB-based SPM result file', and after the first file is loaded this changes to 'Specify Group1 Subject**2** nirsLAB -based SPM result file', *etc*. After the file for the last subject in the first group has been loaded, the title changes to 'Specify Group**2** Subject1 nirsLAB-based SPM result file', *etc*.
  - However, nirsLAB does not compare the names of the files that you select to ensure that they are all of the same hemodynamic state (DeoxyHb *vs*. OxyHb *vs*. TotalHb), or to ensure that you haven't loaded the same file more than once. Carefully examine the name of each file before clicking on the *Open* button, to ensure that you have selected the correct one.

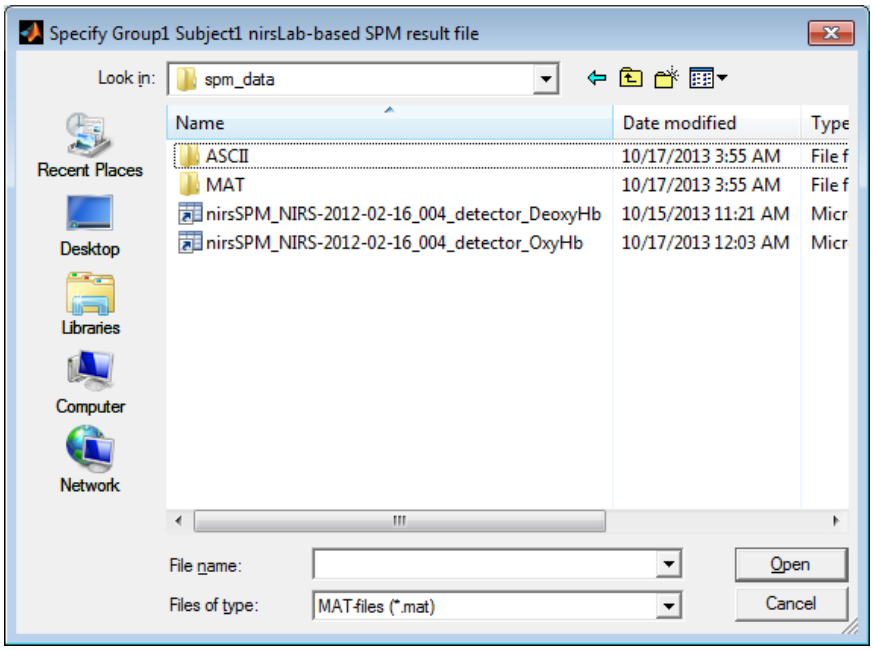


Figure 6-36. The navigator window that is launched when you click on the *Load Multiple data* button (Figure 6-35).

- If the design matrices for different subjects don't all have exactly the same ordering of experimental conditions, then it is necessary for you to re-arrange the columns of the design matrices so that all of them do have the same condition order. To do this, select the 'Yes' radio button near 'Arrange data order:'. This will launch a user interface (Figure 6-37) that allows you to permute the design-matrix columns for selected data sets, in a convenient way.

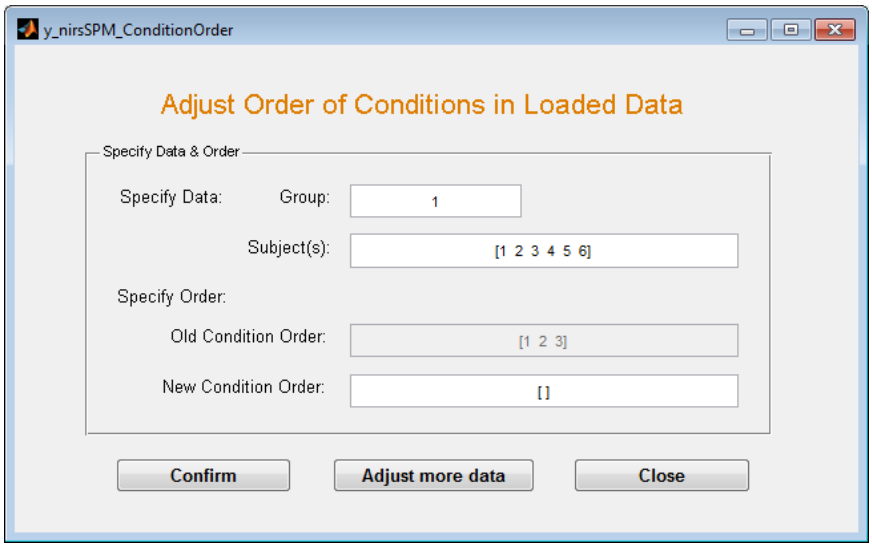


Figure 6-37. The *Adjust Order of Conditions in Loaded Data* GUI, which is launched when you select the 'Yes' radio button in the 'Arrange data order:' line (Figure 6-35).

- Identify which dataset(s) need re-sequencing of design-matrix columns, by entering the group number in the 'Group:' field and the subject number(s) in the 'Subject(s):' field. Note that if two or more subjects in a single group have the same incorrect ordering of design-matrix columns, you may permute the columns of all of their design matrices in one operation.
- In the 'New Condition Order:' field, enter the sequence in which you want to arrange the design-matrix columns, so that they will match the ordering of columns in the design matrices for the other datasets.
- Press the *Confirm* button the implement the re-ordering that you have specified.
- Press the *Adjust more data* button if there are additional datasets with inconsistently ordered design-matrix columns, or *Close* to close the *Adjust Order of Conditions in Loaded Data* window.

2. Specify the F-test contrast matrix or t-test contrast matrix.

- Click on the *Specify Contrast* button in the 'Contrast specification, result visualization' module (Figure 6-38). This will launch the *SPM contrast manager* GUI.

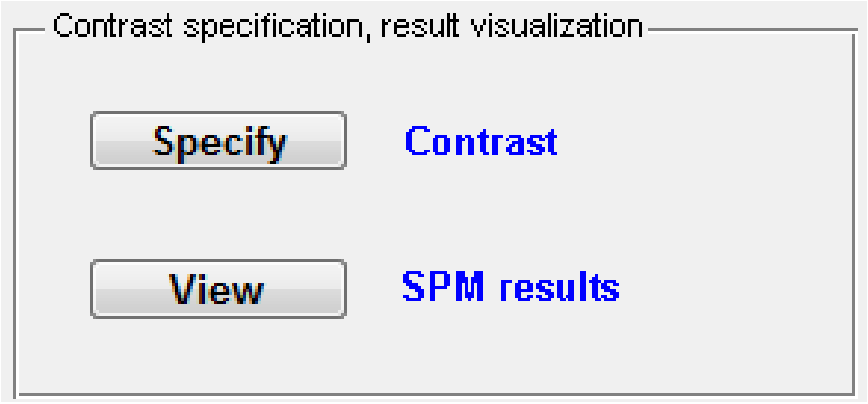


Figure 6-38. Detail view of the 'Contrast specification, result visualization' module of the *Statistical Parametric Mapping Level 2 (between-subjects)* GUI.

- Press the *Define new contrast...* button in the *SPM contrast manager* window. Proceed in the same manner as described above for generating Level-1 SPF{F} images or Level-1 SPF{t} images.
  - The type of biological hypothesis that you will most commonly be evaluating is that an experimental condition, or some combination of conditions, elicits a different hemodynamic response in one group of subjects than in another group. For example, suppose that:
    - Models $x_1(t)$ and $x_2(t)$ tell you when a low-pitched and a high-pitched sound, respectively, were presented to the subjects.
    - One subject group comprises people who play musical instruments professionally, while the other group consists of control subjects who work in other fields.

- You want to know if the difference between the hemodynamic responses to the two sounds is larger in the first subject group than in the second.
- The design matrix for each subject also includes three other temporal models that are not relevant to this hypothesis.
- You would test the preceding hypothesis by specifying

$$\begin{array}{l} 1^{st}\ \text{contrast} \rightarrow \\ 2^{nd}\ \text{contrast} \rightarrow \end{array} \overbrace{\begin{bmatrix} -1 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}}^{\text{Design matrix models for subject group 1}} \overbrace{\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 1 & -1 & 0 & 0 & 0 \end{bmatrix}}^{\text{Design matrix models for subject group 2}} \overbrace{\begin{bmatrix} 0 \\ 0 \end{bmatrix}}^{\text{Constant term in composite (2-group) design matrix}}$$

as the F-contrast matrix.

- Note that it is also permissible to specify a contrast (*i.e.*, an individual row of the contrast matrix) that includes information from both groups. For example, suppose that the biological hypothesis you want to evaluate is that there is a difference between the inter-group response differences for experimental condition 3 and for experimental condition 4. You can test that hypothesis by specifying

$$\begin{bmatrix} 0 & 0 & 1 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 \\ 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \end{bmatrix}$$

as the F-contrast matrix.

- If you are testing a hypothesis involving a simple comparison between two conditions, it may be more appropriate to perform a t-test. For example, suppose that the biological hypothesis you want to evaluate is that there is a difference between the two groups' hemodynamic responses to condition 5. You can test that hypothesis by specifying

$$\begin{bmatrix} 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & -1 & 0 \end{bmatrix}$$

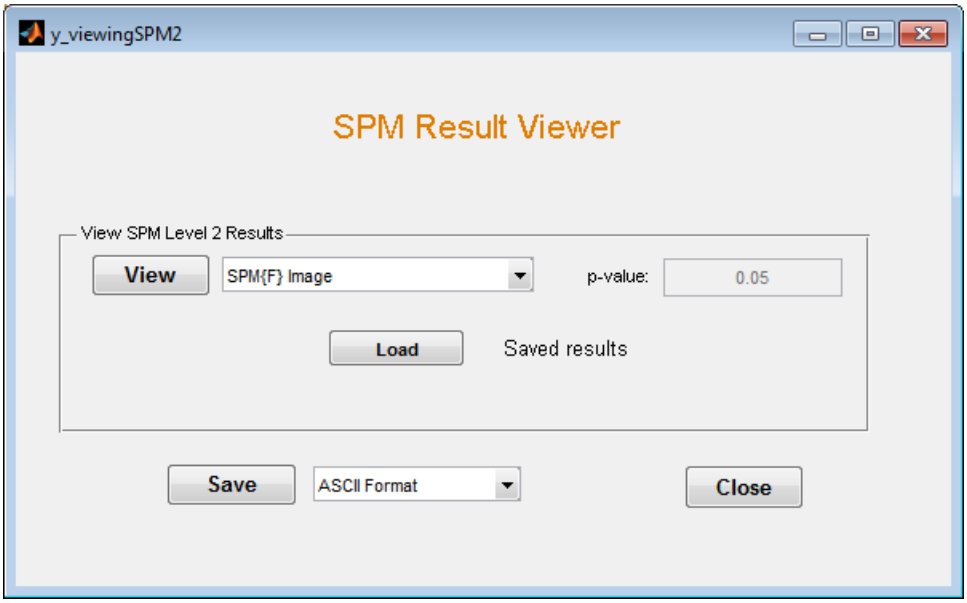
as the t-contrast matrix.

- When you press the *Done* button in the *SPM contrast manager* window, a pop-up window will open asking if you want to save the contrast-generation results (default answer is 'yes'), and suggesting a name for the results file. If you wish, you can modify or replace the file name. Pressing the *OK* button will simultaneously close the pop-up window and launch a navigator window, which you can use to select a folder in which to save the results (default is the current directory of MATLAB).

3. Viewing a SPM{F} or SPM{t} image, or a thresholded SPM{F} or SPM{t} image.

- Press the *View SPM results* button in the 'Contrast specification, result visualization' module. This will launch the *SPM Result Viewer* GUI (Figure 6-39).
- Select an option ('SPM{F} Image', 'SPM{F} Image Thresholded', 'SPM{t} Image', 'SPM{t} Image Thresholded') from the drop-down menu adjacent to the *View* button (Figure 6-39).

- Click on the *Load Saved results* button to launch a browser. Use it to navigate to and select a file containing the Level-2 contrast that you want to view, and press the *Open* button to load it.
  - The only exception to the preceding would occur if you are still in the nirsLAB session in which you generated the Level-2 contrast you want to view, and it is the most recently generated contrast, and you have selected the correct contrast type (*i.e.*, F or t) from the drop-down menu. In this case, you can bypass the *Load Saved results* operation and simply press the *View* button.
- If you selected one of the 'Thresholded' items from the drop-down menu, enter your choice of significance level in the 'p-value:' field.



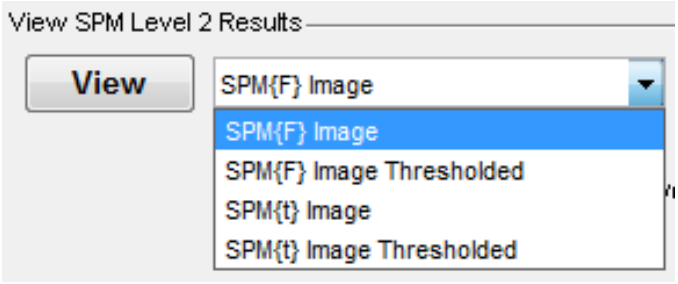
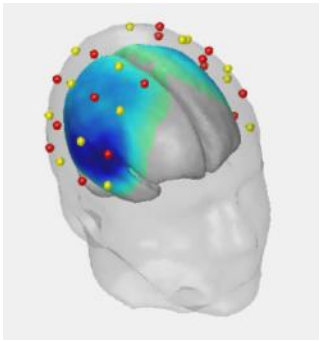
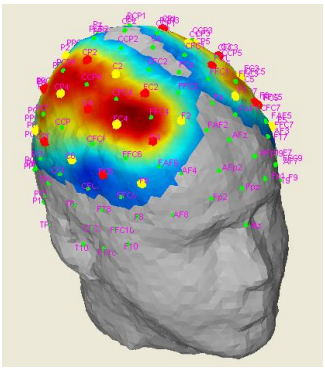
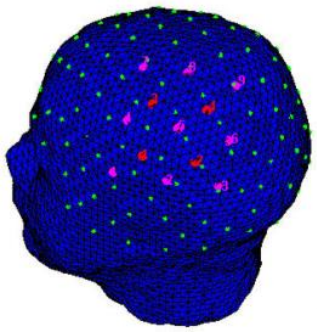
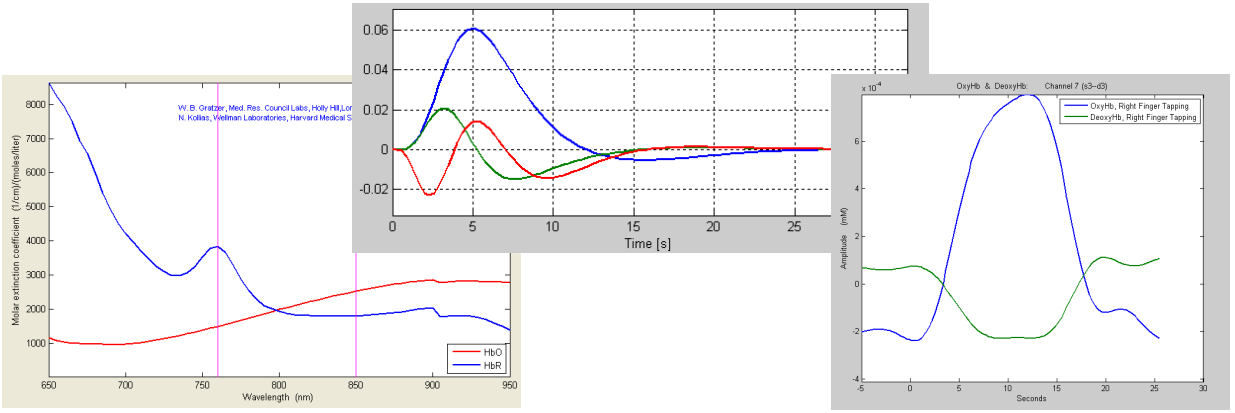


Figure 6-39. (Top) The *SPM Result Viewer* GUI for Level-2 SPM. (Bottom) Detail view of the *View* drop-down menu.

- Press the *View* button. The spatial distribution of the t- or F-statistic you have selected will be displayed in a GUI whose structure and display capabilities are very similar to those of the *MAP Hemodynamic states* GUI of the *Data Viewer* portal (Chap. 5).

If you chose either the 'SPM{F} Image' or the 'SPM{t} Image' option, the displayed image will show you the statistic values in all image voxels. If you chose either the 'SPM{F} Image Thesholded' or the 'SPM{t} Image Thesholded' option, the displayed image will have non-zero values in only the voxels where the test result is statistically significant.

nirsLAB

Chapter 7: Probe Setup

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1 Introduction

The **Probe Setup** module in the **Utilities** portal provides the functionality to specify your experimental optode layout applied to the head surface (*i.e.*, source-detector configuration) and assignment of selected source-detector channels for subsequent viewing and processing. There are two ways to specify the layout: 1) graphically through use of a mouse; 2) by loading a file containing the optode and fiducials coordinates obtained using a 3D digitizer such as the Polhemus Patriot 3D Tracking System. A similar approach is available to specify channel assignments. This module also provides visualization utilities to view or edit existing or newly generated optode layouts.

1.1 Launching Probe Setup

Take the following steps to launch the **Probe Setup** module:

First, select the 'Setup probes' option, shown in Figure 7-1, through the pull-down menu listed in the nirsLab **Utilities** portal.

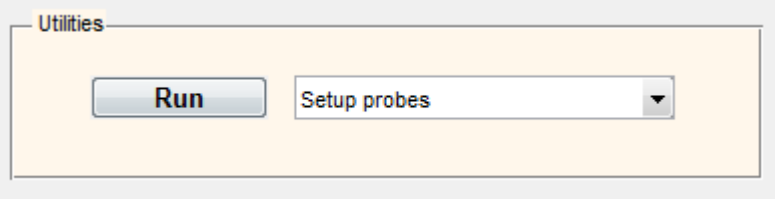


Figure 7-1. Probes Setup portal.

Next, click the 'Run' button to open a GUI that provides options for specifying the optode layout. The GUI, shown in Figure 7-2, contains four basic components:

Specify S/D Positions: Three options are available – 'On 10-10 system', 'Arbitrary positions', and 'Load S/D positions'.

Assign NIRS Channels: Two options are available – Channel assignment by graphical entry; Channel assignment using a text file.

View Probe/Channels setup: This allows the user to display an existing or newly generated Probe and NIRS channel layout.

Save and close probe setup.

1.2 Specify Source/Detector Positions

There are two options available to specify a source-detector layout. In one case, you can load a preexisting file that contains the coordinates for the optodes and fiducial positions that were generated using a 3D digitizer. The other is to generate these locations using graphical tools provided by a GUI that

is opened when the '*Set*' Source Positions button is activated. Graphical specification can be accomplished by mapping probe locations to the International 10-10 system convention or by specifying arbitrary locations using the listed radio button. To load a file from a digitizer, the user selects the '*Load S/D positions*' button.

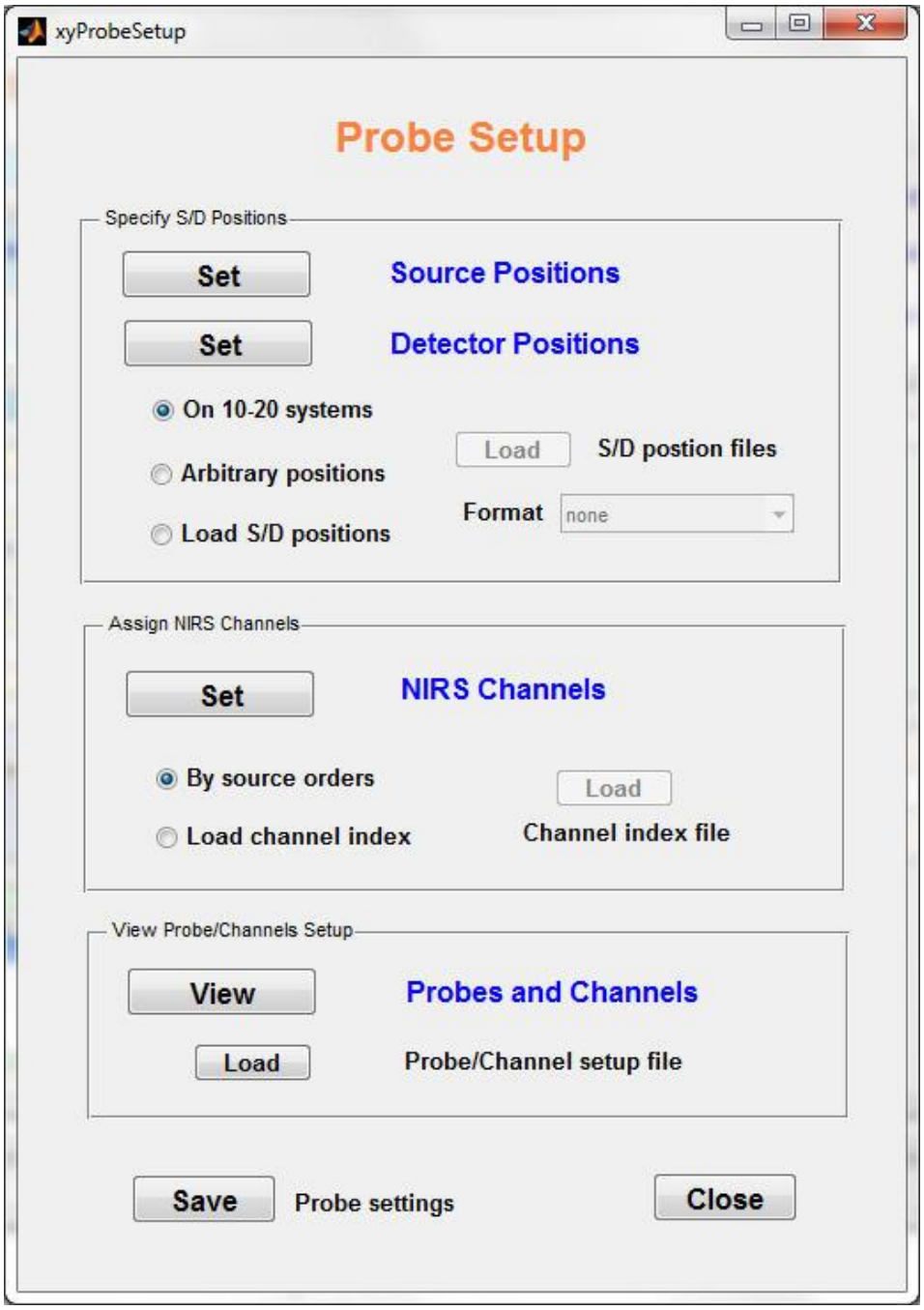


Figure 7-2. GUI for Specifying Probe Setup

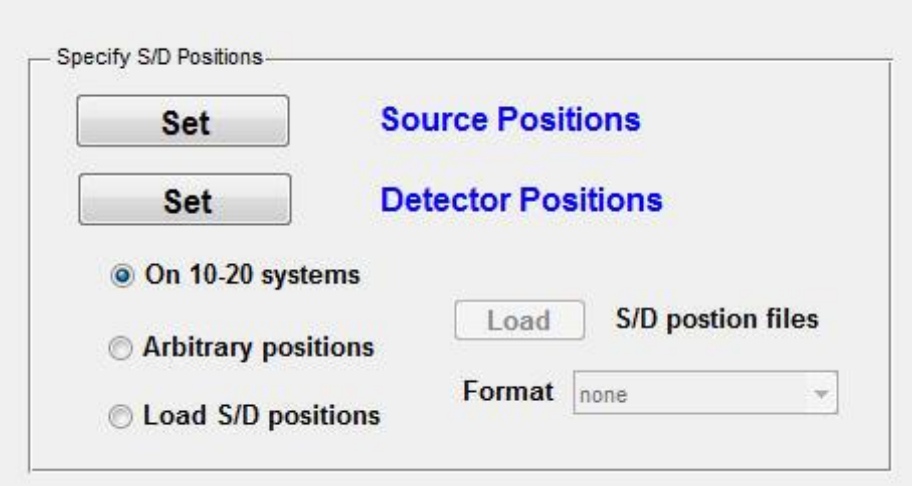


Figure 7-3. Portal for specification of optode

Shown in Figure 7-3 are functions accessible under the '**Specify S/D Positions**' portal. The default setting is the 10-10 system. Activation of the '*Set*' Source Positions button will open the GUI shown in Figure 7-4.

1.3 Setting Source Positions

The GUI shown in Figure 7-4 has three principal functional fields plus a graphical display field. The latter includes displays based on either a 2D planar view or 3D head model on which are indicated the standard 10-10 EEG positions. User directed operations include: (1) specification of number of sources; (2) graphical indication of source locations; (3) file saving and closing of GUI.

As annotated in the Figure, having first indicated the number of sources (1), next the user will click on the '*Set*' button located at the top-left portion of the GUI (2). Should the user forget to enter a non-zero source number, or incorrectly enter a non numeric character, clicking on the '*Set*' button will open a reminder pop-up that a corrected value should be entered. Having correctly specified a positive integer, this will allow the user to navigate with the mouse to desired locations within the map. Left clicking of the mouse at desired positions will highlight the location and label the source number.

Figure 7-5 shows an example of this labeling for the case in which eight source locations were identified.

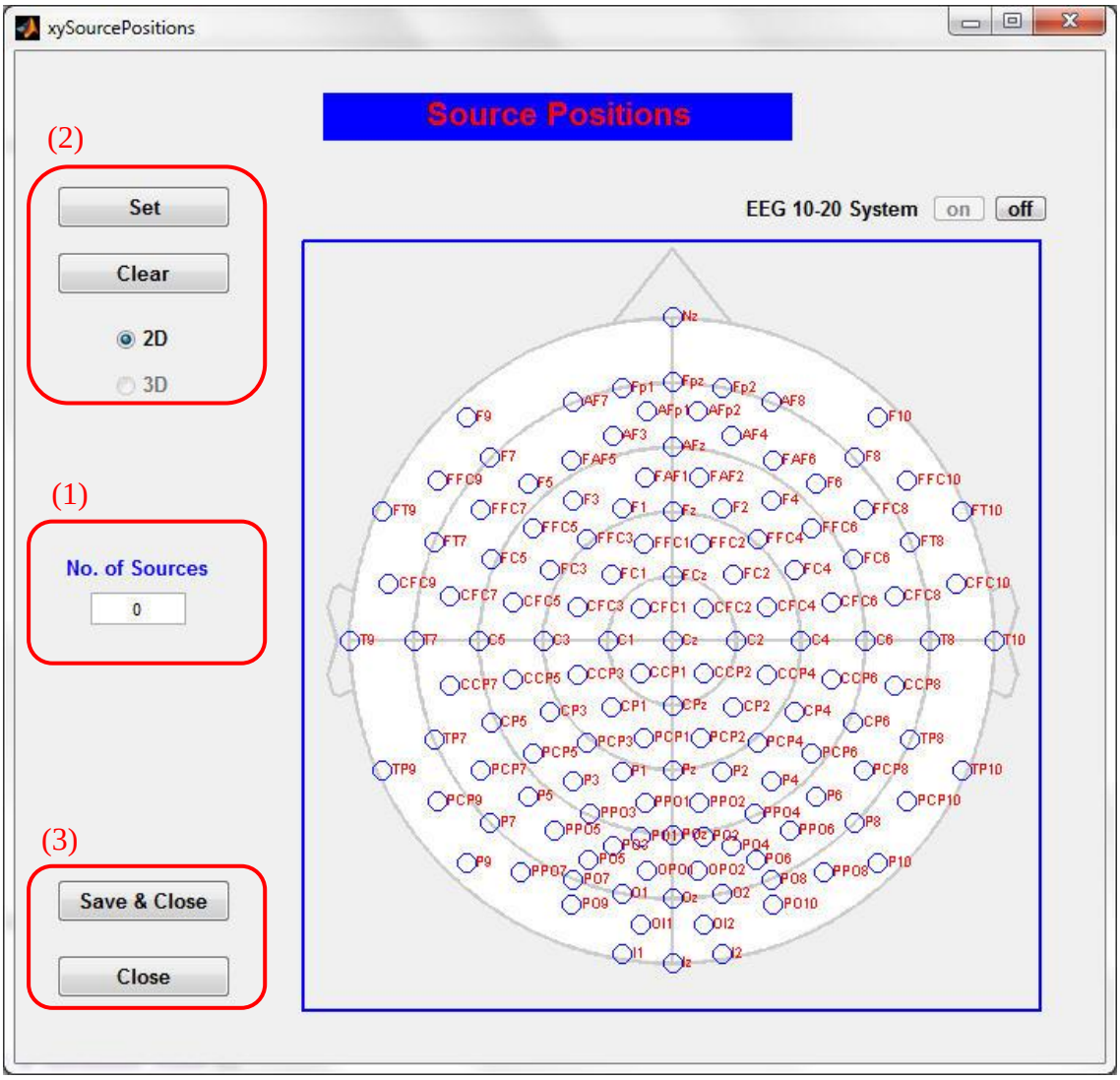


Figure 7-4. GUI for specification of probe layout.

Steps: Click the '*Set*' button in the upper left corner and move the mouse cursor onto the first source position, and click the primary mouse button. Then move the cursor onto the next source position and click the primary mouse button again. Repeat this process until all sources are specified for the probe setup. If you make a mistake during setting of the source positions or want to delete a source location you already have set, click the '*Clear*' button under the '*Set*' button to delete the most recently set source position. Then click the '*Set*' button again to continue setting source positions.

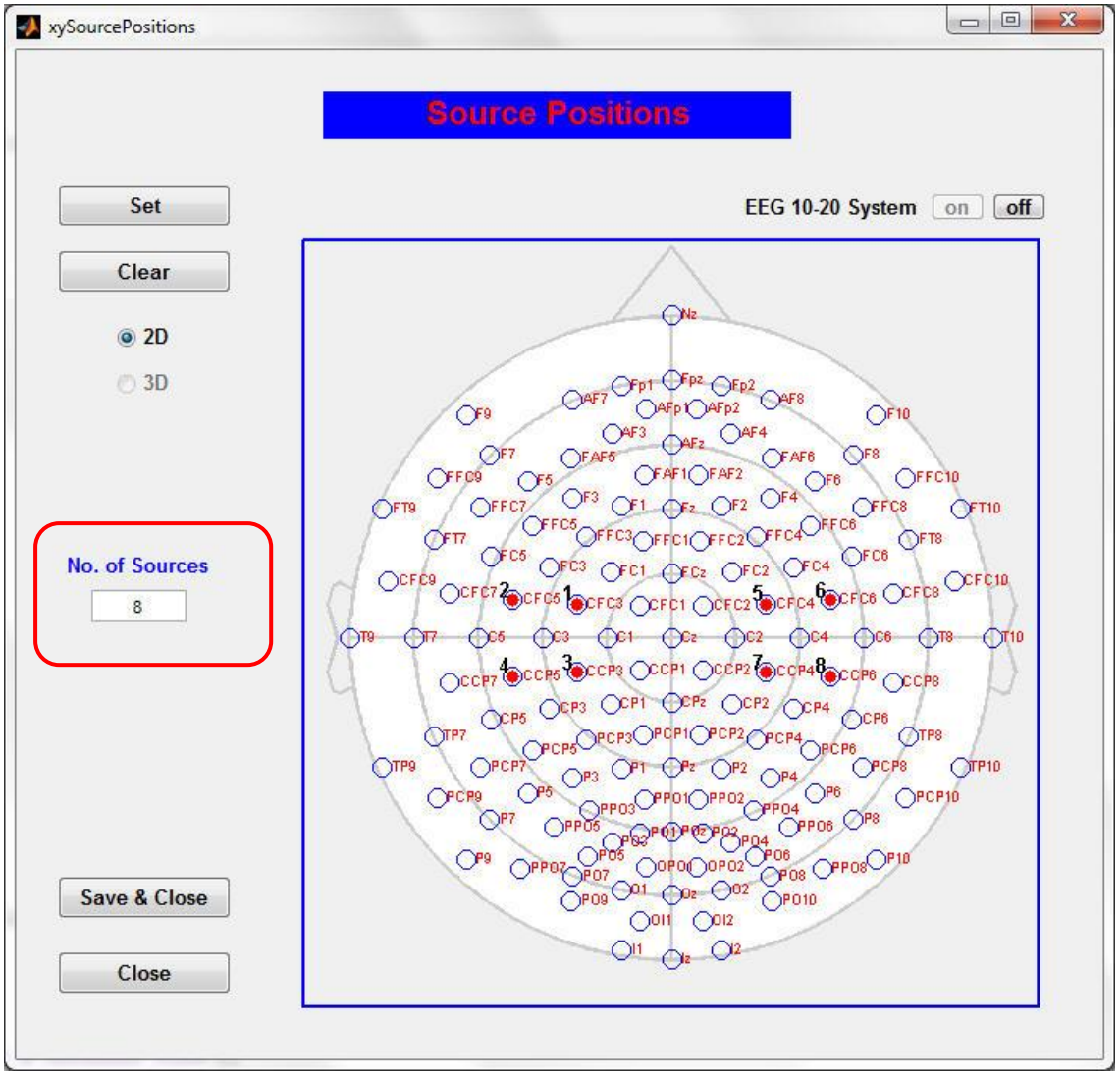


Figure 7-5. GUI showing positioning of 8 selected source locations.

Having correctly completed specifying the source positions, the user will now click on the '*Save& Close*' button in the lower left corner of the Source Positions GUI. After clicking the button, a browser window shown in Figure 7-6 will be opened for specifying the folder and file name to save your probe setting. As an example shown below, the file is named as 's8d18', and the folder '18_6_2013' is selected to store the file. After clicking the Save button, your probe setting is saved as 's8d18_probeInfo.mat' in the folder you selected, and a help dialogue window will open that identifies where the name and location of the stored file (Figure 7-7).

Note that the file name will automatically be ended with '_probeInfo.mat'. This file will be called as probeInfo file, and it contains the geometric information of the probes you specified.

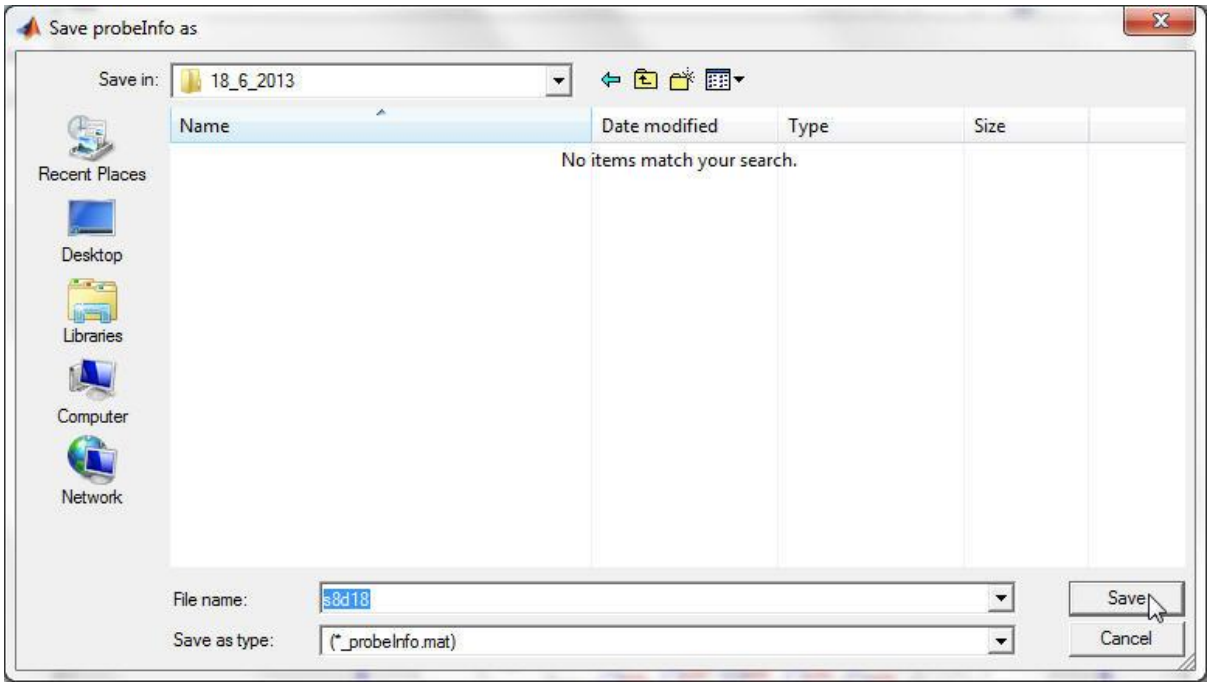


Figure 7-6. Browser window for specifying source settings.

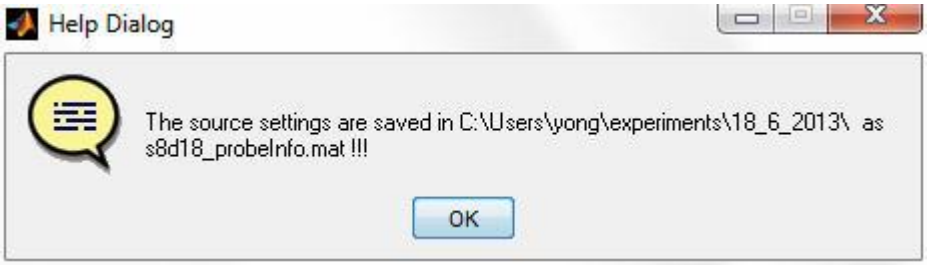


Figure 7-7. Help Dialog indicating file location and name.

1.4 Setting Detector Positions

The steps for setting detector positions are parallel to those given above for setting source positions.

Step 1: Clicking the 'Set' button next to the words '*Detector Positions*', as illustrated in Figure 7-8, brings up a new GUI entitled 'Detector Positions' shown in Figure 7-9.

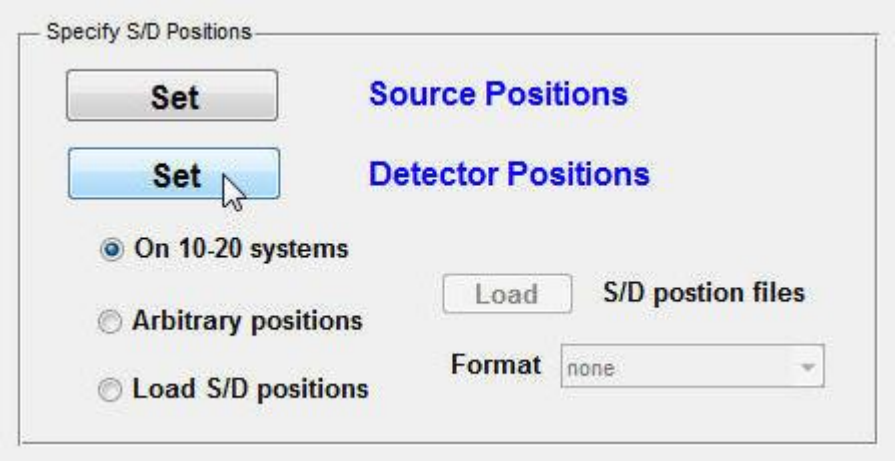


Figure 7-8. Selection of 'Set' Detector Positions.

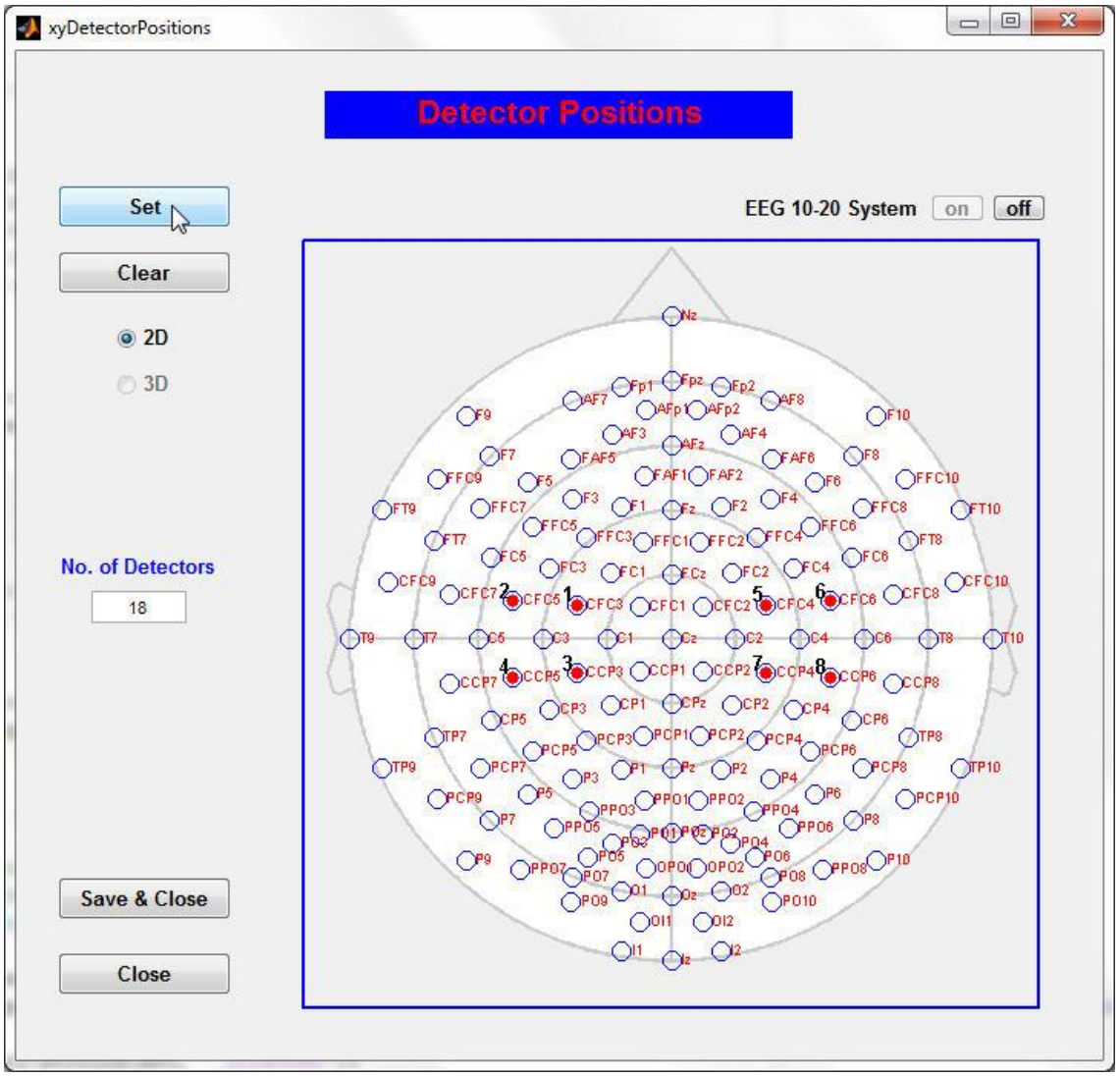


Figure 7-9. GUI for specification of detector locations.

As seen in the figure above, the source positions set previously have been also marked by red dots in the Detector Positions GUI.

Step 2: Type the number of detectors used in data collection by entering the value in the '*No. of Detectors*' field located in the left middle area of the Detector Positions GUI.

Step 3: Click the **Set** button in the upper left corner, move the mouse cursor onto the first detector position, and click the primary mouse button. Then move the cursor onto the next detector position and click the primary mouse button again. Repeat this process until all detectors are specified for the probe setup.

Shown in Figure 7-10 is an example of a completed detector-positions settings, where 18 detector positions were set and are marked by blue dots.

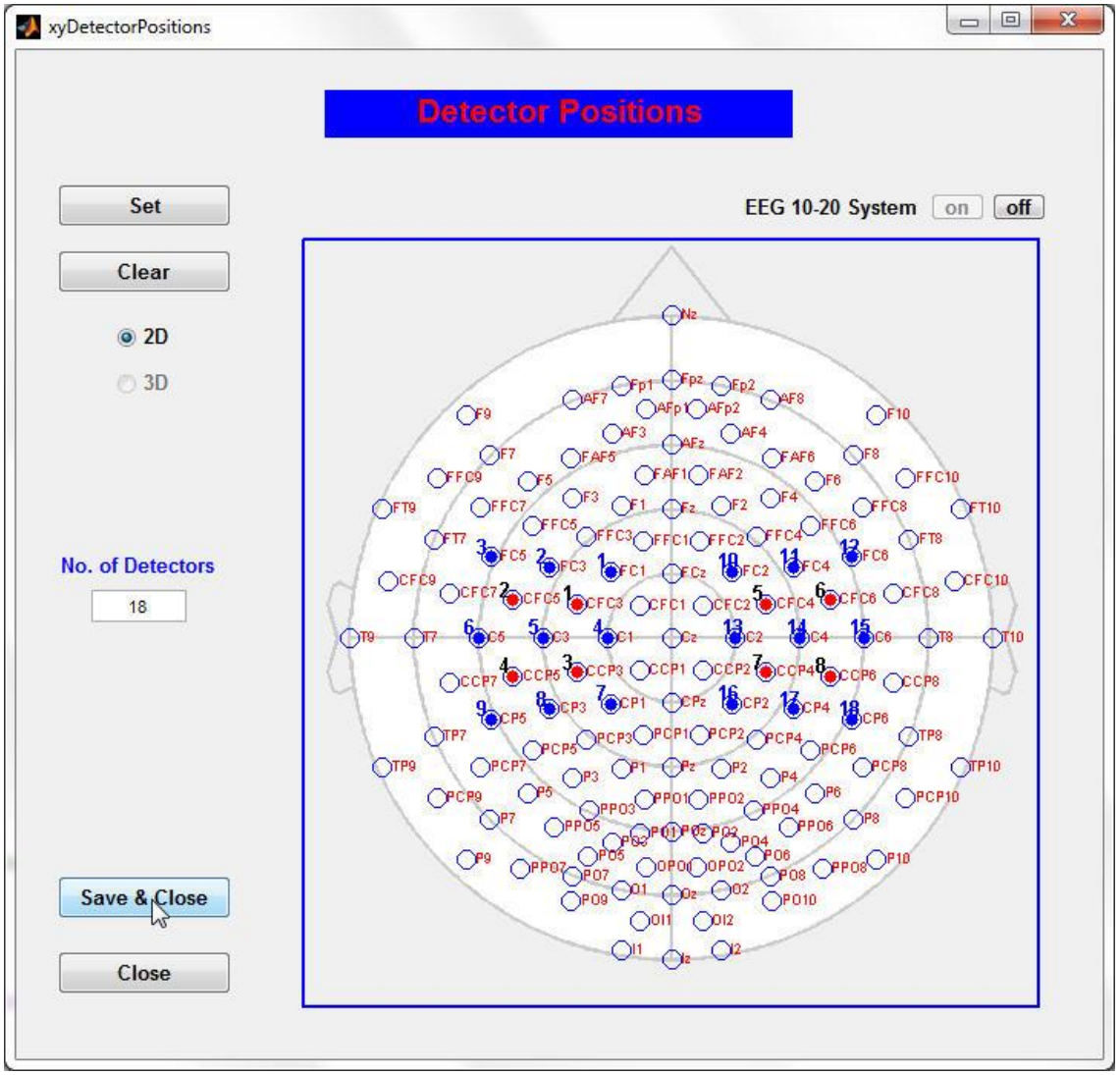


Figure 7-10. Graphical specification of detector locations.

Step 4: Clicking the '*Save & Close*' button in the lower left corner of the Detector Positions GUI, will save the detector settings in same folder you selected for the source positions. When done, a help dialogue window shown in Figure 7-11 will open, identifying file name and location.

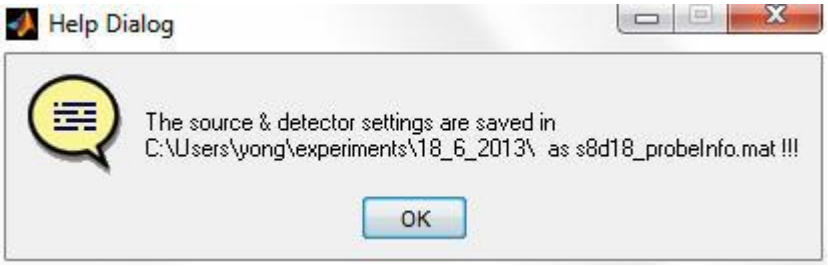


Figure 7-11. Help dialogue identifying detection settings file.

1.5 Arbitrary Probe Positions

When the sources and detectors were not all arranged in accordance to the EEG 10-10 system, specification of probe locations that are arbitrarily positioned is made following activation of the '*Arbitrary positions*' radio button as shown in Figure 7-12. The approach for specifying the source and detector locations is made using an identical approach as with the 10-10 positions with the exception that clicking of the mouse to an arbitrary location in the display field highlights its position.

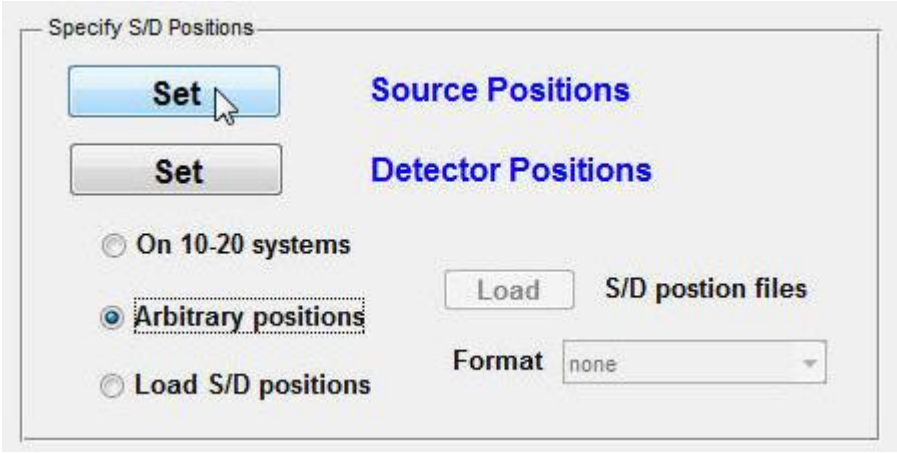


Figure 7-12. Specification of arbitrary probe locations.

1.6 Specification of probe location using a 3D head model

So as to provide for a more realistic view of assigned probe locations, the above indicated steps applied to 2D mapping can be also be used with a 3D head model. The selected head model shown corresponds to a MRI image obtained from an arbitrary adult male. Similar to the 2D mapping method described above, specification of probe location using the 3D head model can be made using the 10-10 system or

by specifying arbitrary locations. To facilitate assignments, features for rotating the image and a labeling of preset locations in accordance with the 10-10 system are provided. Figures 7-13 and 7-14 shows screen shots for a case where 4 sources and 9 detectors were specified in the vicinity of the left motor cortex.

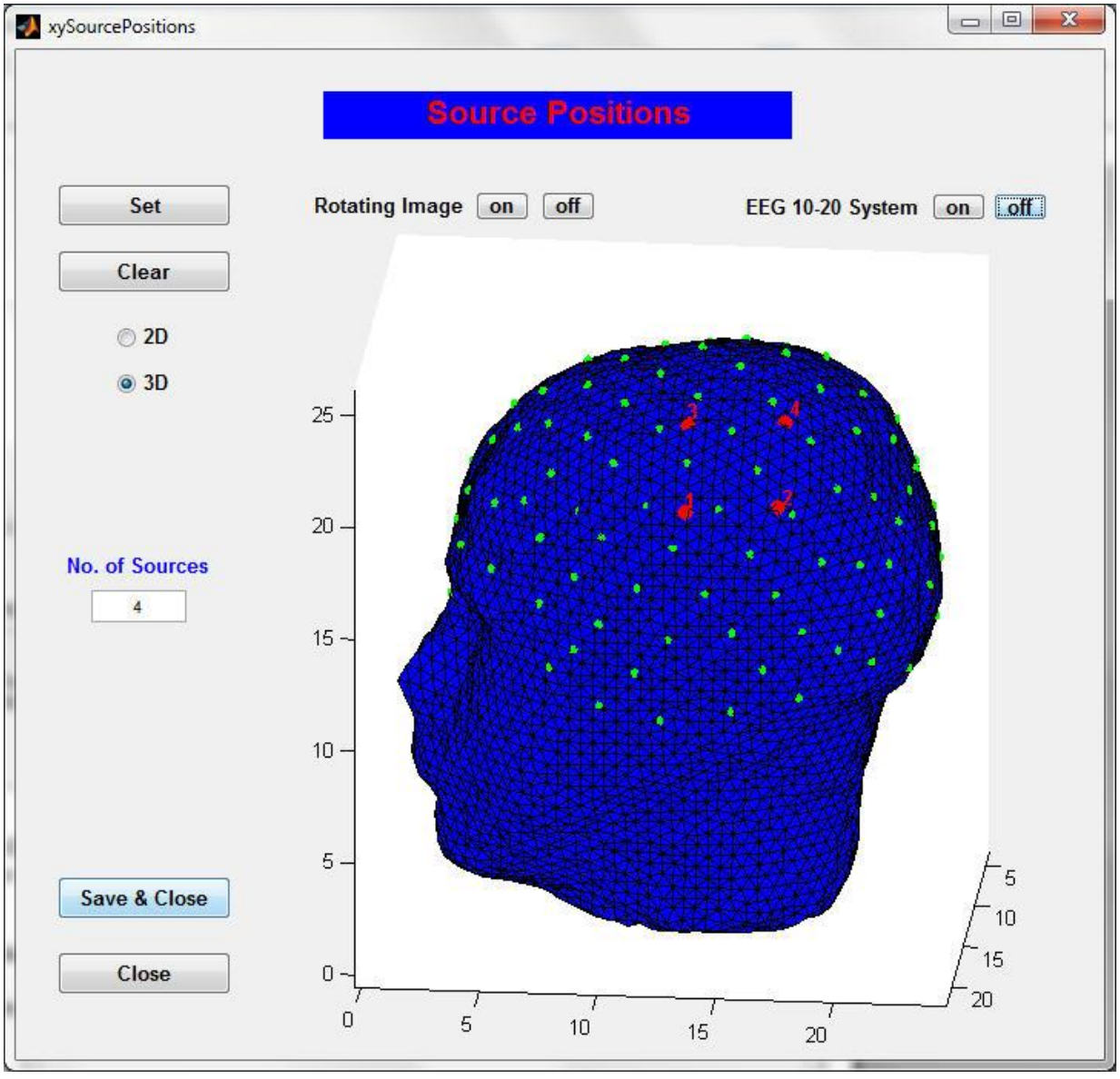


Figure 7-13. Probe positions for 4 assigned source locations.

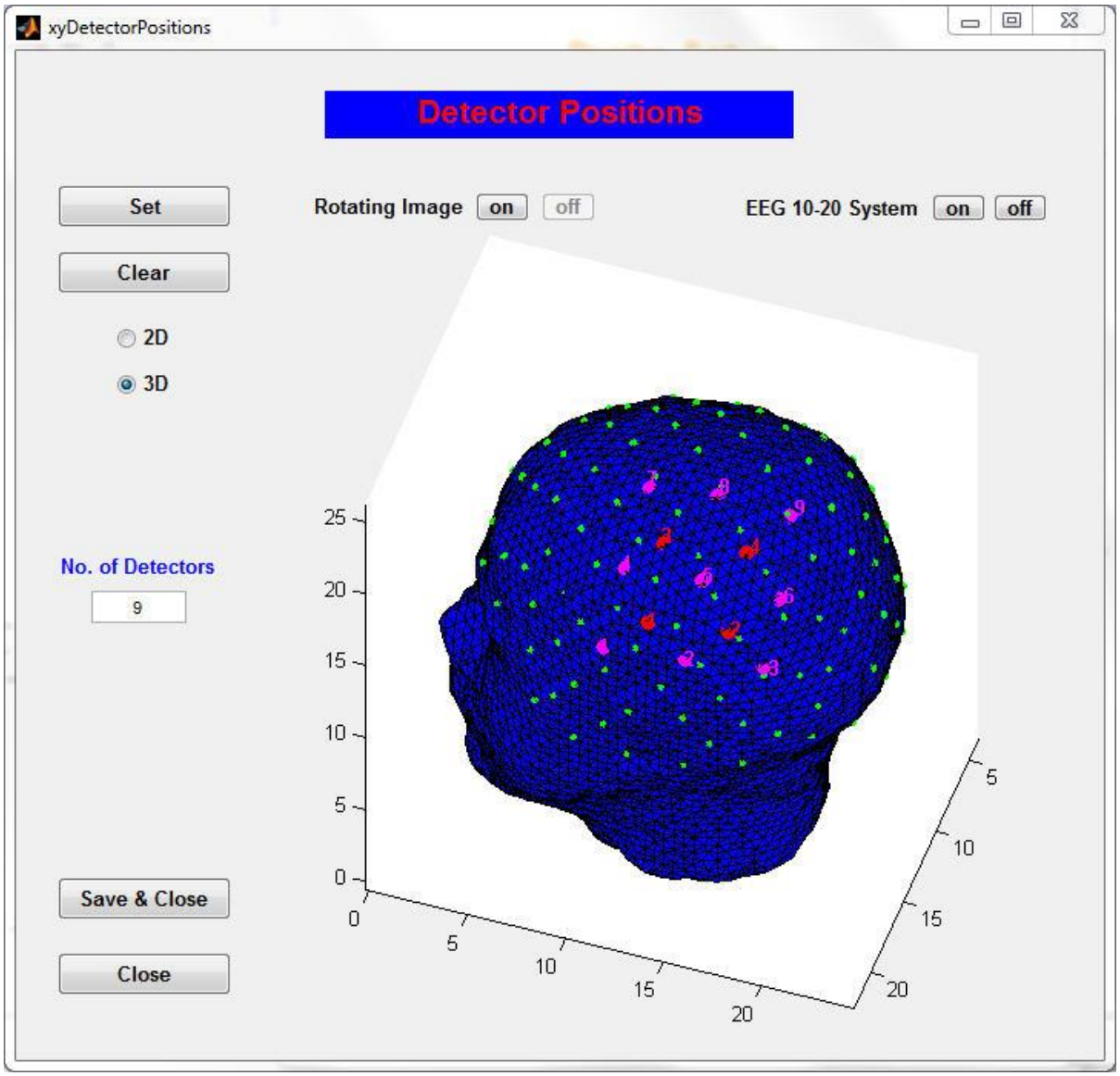


Figure 7-14. Probe locations for 9 assigned detector locations.

1.7 Load source/detector positions obtained using a 3D Digitizer

Specification of locations of the sources, detectors and fiducial points with a 3D digitizer can serve to accurately map sensor data to the head space. Clicking the radio button of '*Load S/D positions*' in the Probe Setup GUI seen in Figure 7-15 will active the *'Load'* button and the ***'Format'*** pull-down menu.

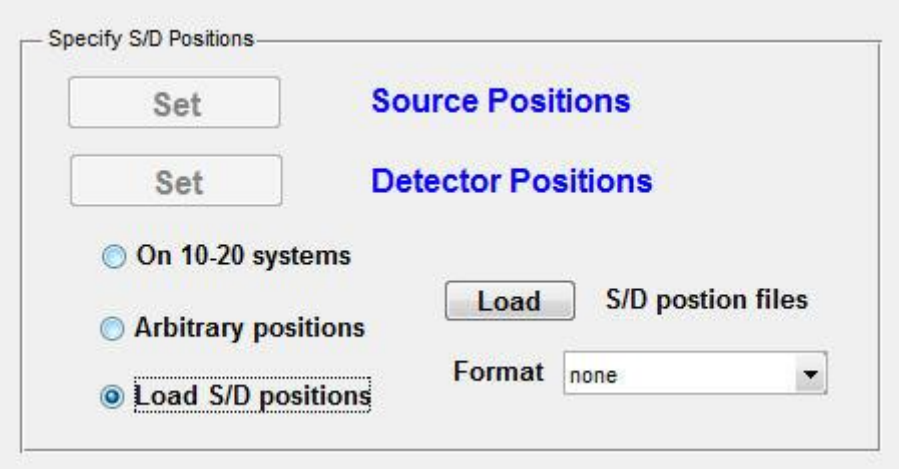


Figure 7-15. Loading of files from a digitizer.

Steps to specify source and detector positions by loading their coordinate files are as follows:

Step 1: First select the format of the coordinate files you will load. Click the '*Format'* pull-down menu, shown in Figure 7-16, will reveal two options: PATRIOT (Polhemus) and User-defined.

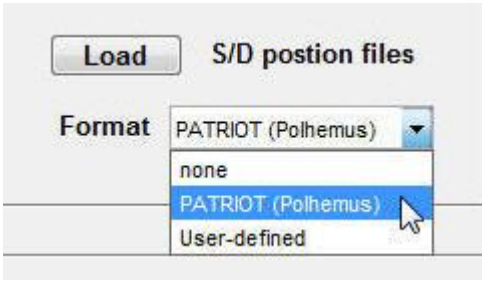


Figure 7-16. Specification of Patriot Data

The probe setup toolbox presently only directly reads measured data format from Polhemus Patriot 3D Tracking System. To load data obtained from other 3D digitizing systems you will need to edit your data into the User-defined format, then choose the User-defined in the '*Format'* pull-down menu. A detailed explanation about the User-defined format is given in Appendix A following this section.

Step 2: Click the '*Load'* button next to the words '*S/D position files*' to open a browser window, which you will use to navigate to the folder where the files containing the measured source, detector and fiducial point coordinates are stored. Sequentially open the measured fiducial-point coordinates first, then the detector coordinates, and finally the source coordinates, as shown in Figure 7-17.

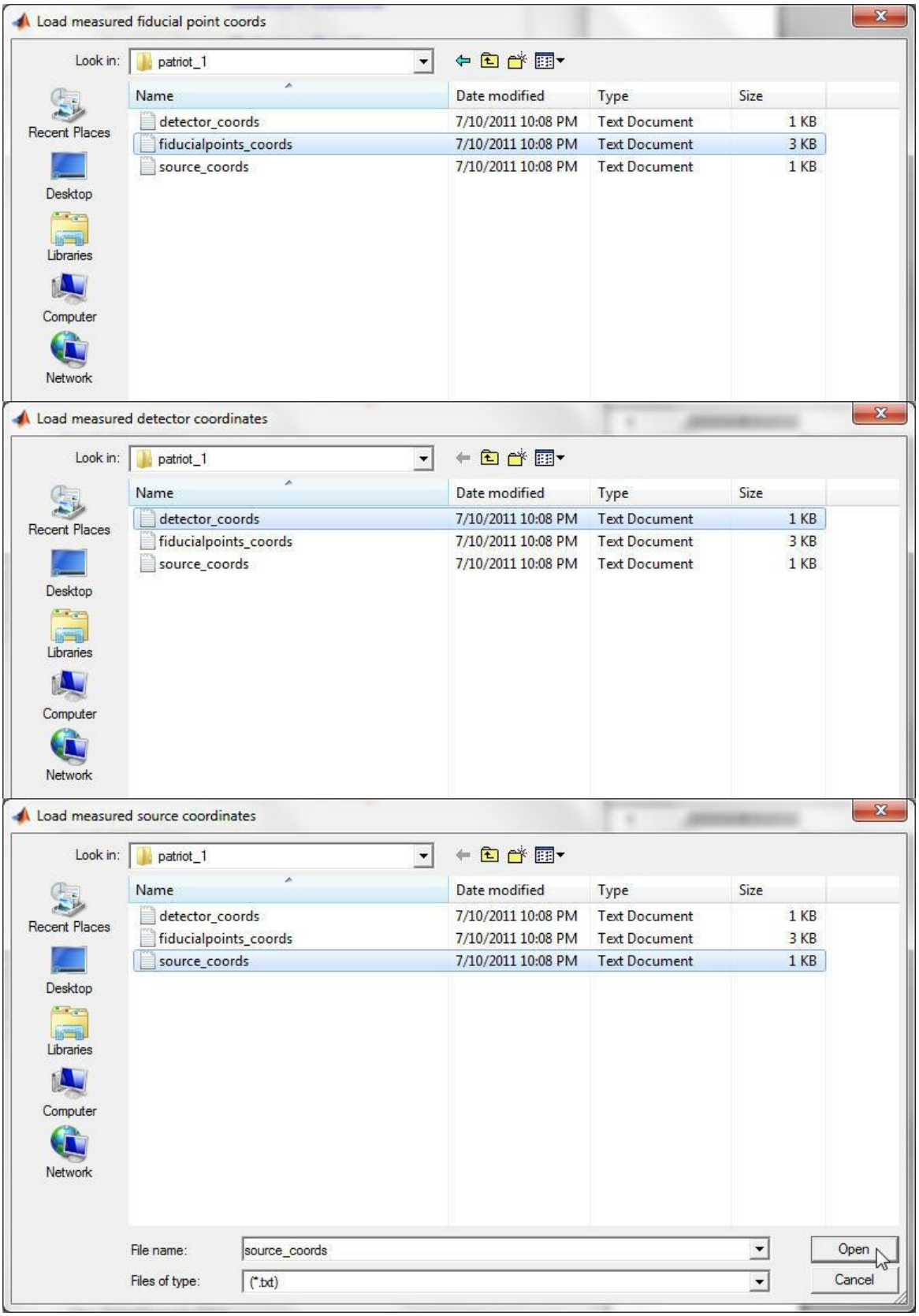


Figure 7-17. Sequential loading of coordinate files.

After the three measured coordinate files are loaded, the measured source/detector coordinates will be automatically registered onto the NIRx image atlas via an affine transformation. As explained in Appendix B, this algorithm makes use of thirteen fiducial points comprising the two principal axes of the head; left to right preauricular, nasion-inion. As listed in the appendix are the definitions and measuring order of these points.

When file loading and the source/detector registration are completed, a help dialogue window opens, shown in Figure 7-18, that indicates that the coordinate files have been successfully loaded and remind you what is the next step for the probe setup.

Help Dialog
The source and detector coordinates have been successfully loaded and co-registered onto the NIRX atlas.Please go to the next step: "Set" NIRS channels!
OK

Figure 7-18. Help dialogue confirming successful sensor

1.8 Appendix A: User-defined data format

The user-defined source, detector and fiducial point coordinate files are simple text files that identify the respective spatial coordinates of a corresponding data type.

The following matrix shows an example of a user-defined source coordinate file. This is a 8 by 3 matrix, which means there are 8 source positions that have been measured; each row contains x, y and z coordinates of a source position on the subjects head in relation to a defined laboratory reference point.

16.3424	11.6921	24.1230
18.2655	11.6740	22.7233
19.8216	11.6668	20.9953
17.4352	12.7076	23.5153
19.1421	12.5019	22.0111
16.5415	13.3793	24.2306
18.4334	13.3745	22.9074
19.8593	13.3225	21.1122

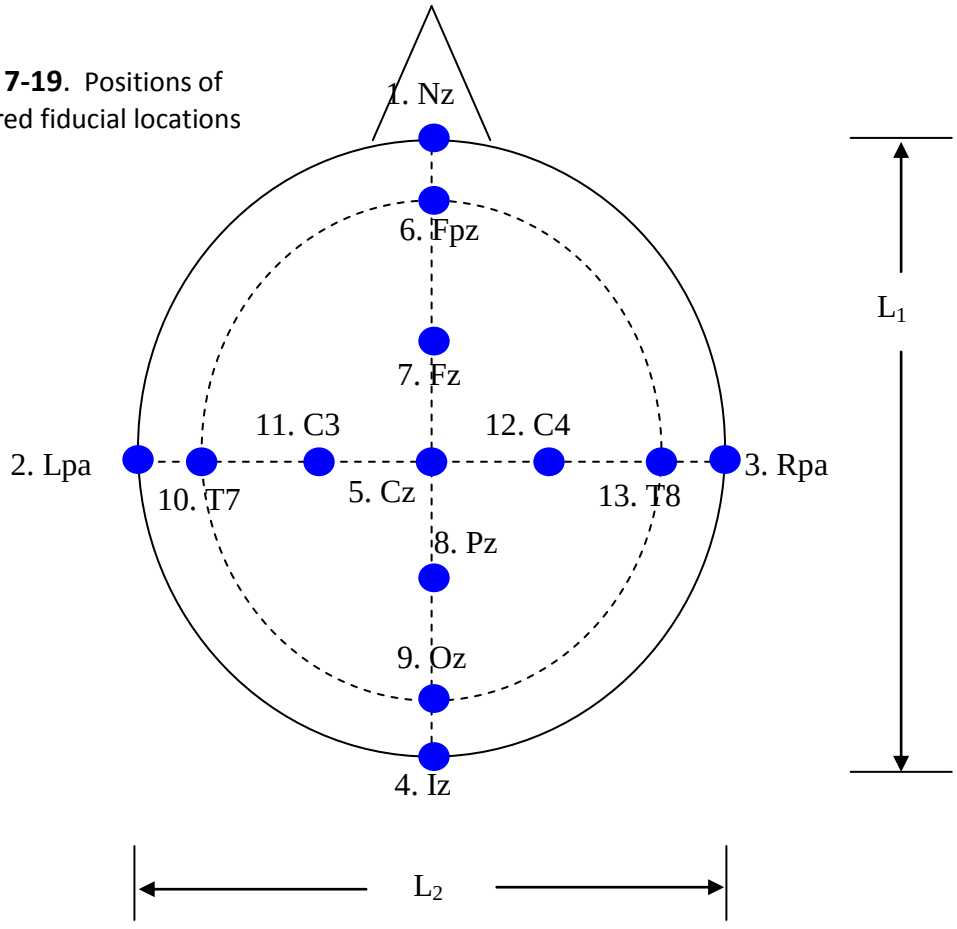
Note, that when you generate the user-defined data files, you must make sure that the coordinates in the files are in same reference frame and same unit (cm). Similar files are generated for the detector and fiducial coordinates.

1.9 Appendix B: Definition of fiducial points

In order to generate the affine transformation matrix for source/detector registrations, thirteen EEG 10-20 system points are selected as the fiducial points in this probe setup toolbox as shown in Figure 7-19. The definition and measuring order of the thirteen fiducial points are as follows:

1. Nz (Nasion)
2. Lpa (Left pre-auricular, T9)
3. Rpa (Right pre-auricular, T10)
4. Iz (Inion)
5. Cz Length(Nz, Cz)=0.5 L_1 and Length(Lpa, Cz)=0.5 L_2
6. Fpz Length(Nz, Fpz)=0.1 L_1
7. Fz Length(Nz, Fz)=0.3 L_1
8. Pz Length(Nz, Pz)=0.7 L_1
9. Oz Length(Nz, Oz)=0.9 L_1
10. T7 Length(Lpa, T7)=0.1 L_2
11. C3 Length(Lpa, C3)=0.3 L_2
12. C4 Length(Lpa, C4)=0.7 L_2
13. T8 Length(Lpa, T4)=0.9 L_2

Figure 7-19. Positions of measured fiducial locations



Where L_1= Length(Nz, Iz) is the length between Nz and Iz, and L_2=Length(Lpa, Rpa) the length between Lpa and Rpa, as shown below. When you measure the fiducial point positions by a digitizing system, or generate a user-defined fiducial coordinates file, you must follow the order of fiducial points. Otherwise registration of source/detector array will be incorrect.

2.0 Assigning of NIRS Channels

Located in the middle of the Probes Setup GUI is the **Assign NIRS Channels** portal, shown in Figure 7-20, that provides for specification of the NIRS channels. A NIRS channel is defined as a source-detector pair. Spatially, these are assigned to the position mid-way between a selected source and detector. Careful consideration is warranted when selecting channels as many of the display and data transformation features in nirsLAB are intended to operate only on these selected channels. So as to provide for maximal flexibility in experimental design and optode layout, NIRx imagers are designed to obtain a parallel readout of all detector responses at each illumination event, irrespective of the location of any source unless otherwise specified. Depending on the density of the optode layout employed, this can result in some detectors being located at distances too large to distinguish optical intensities from noise. The intent of the *Assign NIRS Channel* operation is to restrict consideration of the measured source-detector responses to only those likely to yield useful signal-to-noise ratio. In most instances, this means source-detector pairs only within 4 cm of each other are assigned.

Note, that in cases where the probe density includes multi-distance measures, it can be advantageous to generate more than one specification of assigned NIRS channels (*e.g.*, layout of near detector responses, layout of far detector responses).

For a considered layout, there are two ways to set NIRS channels: '***By source order'*** and '***Load channel index***'. These are implemented by activating the respective radio button.

Figure 7-20. Options for specification of NIRS channels.

2.1 By source order

As the name infers, the features accessed through the '*By source order*' radio button, assigns channels in an incremental fashion in accordance with the source number (*i.e.*, S_1, S_2, S_3 …). Clicking on the '*Set*' button in Figure 20 will open a new GUI, shown in Figure 21 that has a layout and functionality nearly

identical to the Source and Detector Positions GUI. The default view is a color coded map (red- sources, blue- detectors) of assigned source-detector locations (see, section 1.2 in this chapter) that are viewable in either a planar (2D) or head-surface (3D) view.

Clicking the set button in this GUI will: (i), display the location of Source 1, (ii), activate movement of the slider for subsequent identification of other source positions, and (iii), provide for a cross-hair that, upon clicking on desired detector locations, will select the associated NIRS channels. NIRS channels are assigned in a consecutive sequence with each chosen source-detector pair. In the case of optode layouts having spacing on the order of 3 cm, channel assignment is normally limited to detectors that are the nearest neighbors. Clearing of an incorrect assignment is made by clicking on the '*Clear*' button followed by the '*Set*' button to allow for continued assignment. Upon completion of channel assignment for Source 1, access to other source positions for respective assignments is made by indexing the slider

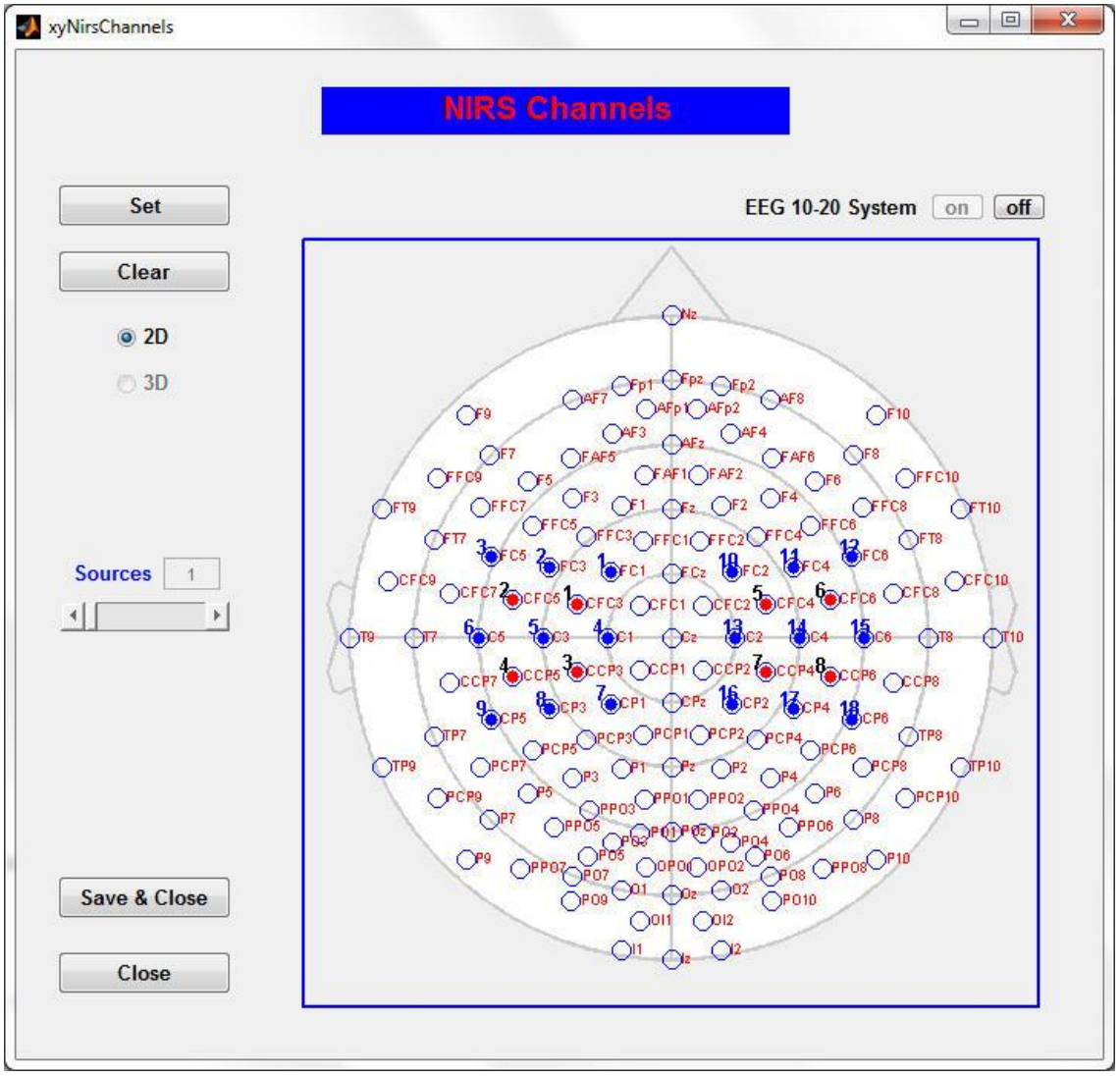


Figure 7-21. NIRS channel assignment GUI.

and repeating the steps mentioned. An example of assigned channels for detector positions that are nearest neighbors to Source 1 is shown in Figure 7-22. Note, so as to provide viewing clarity, with each chosen source a new screen appears absent of the previous assignments.

Review and additional editing of assigned channels is available for each source by indexing the source scroll bar. Upon completion of channel assignments, clicking of the '*Save and Close*' button will generate a .mat file that is saved and opens a Help Dialog, (example shown in Figure 7-23) that confirms file location.

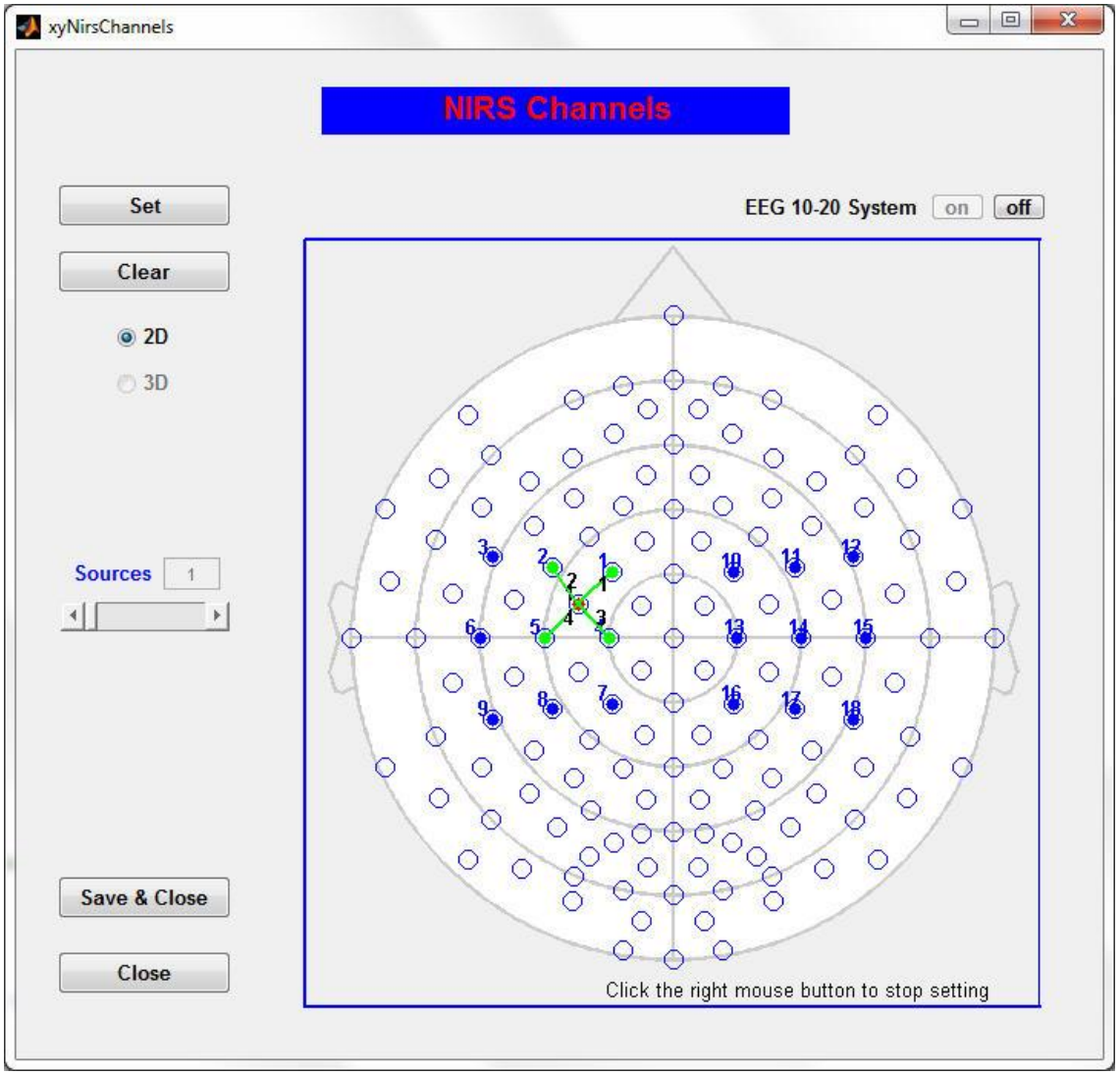


Figure 7-22. Nearest neighbor channel assignment for Source 1.

Figure 7-23. Exemplary Help Dialog window identifying location of saved probe settings.

2.2 Load channel index

This functionality supports channel assignment by way of a text file containing source and detector index information. The data format consists of two columns; column 1 (left) are source assignments, column two (right) are detector assignments. Figure 7-24 shows and example of the indexing assignments for the source-detector layout illustrated on the left side of Figure 7-21.

```
1  1
1  2
1  4
1  5
2  2
2  3
2  5
2  6
3  4
3  5
3  7
3  8
4  5
4  6
4  8
4  9
```

Figure 7-24. Data format for channel assignment using a text file.

As shown in Figure 7-25, to access this functionality first activate the '*Load channel index*' radio button and then click on the '*Load*' button to open a browser window to gain access to the stored channel index file (example shown in Figure 7-26).

Figure 7-25. GUI access to load assigned channel text file.

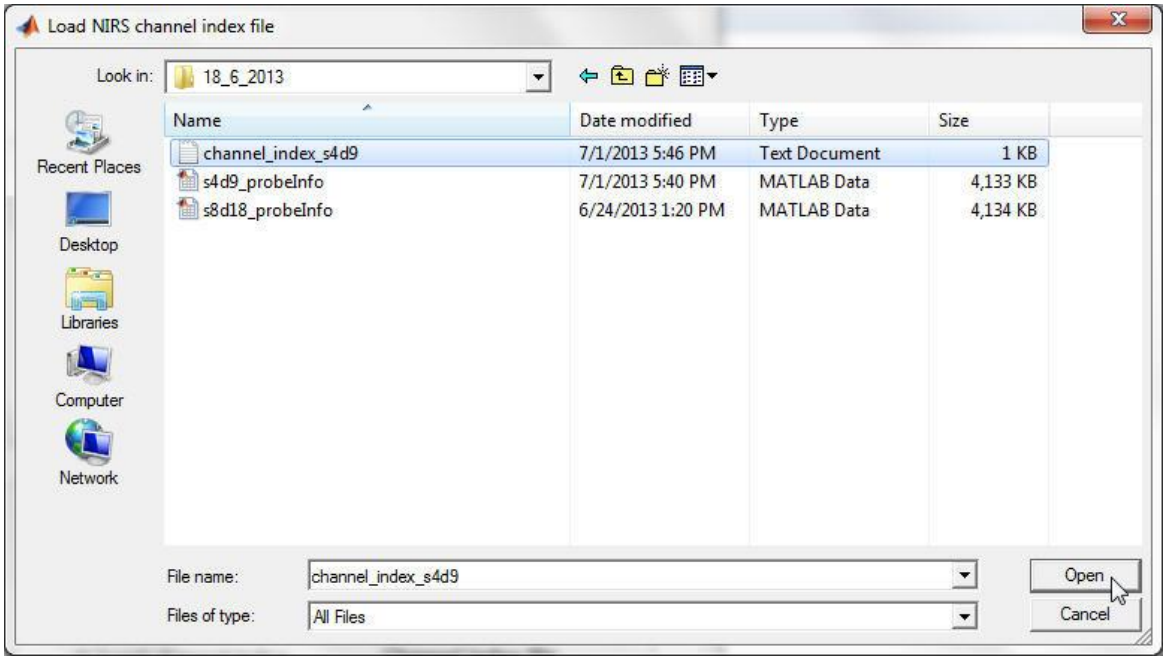


Figure 7-26. Browser window to access Channel index file.

After the channel index file is successfully loaded, the NIRS channels will be automatically assigned according to the channel indices specified. Also activated is a help dialogue window, shown in Figure 7-27, indicating that the NIRS channels have been successfully set and reminds the user what is the next step for the probe setup.

Help Dialog
The NIRS channels have been assigned and saved automatically.Please go to the next step: "View" Probes and Channels !
OK

Figure 7-27. Help dialog identifying channel assignment.

3 View probes and channels

The **View Probe/Channel Setup** panel in the **Probe Setup** GUI, provides utilities to examine a pre-existing probe setup or one newly generated.

If you have just finished setting the probes and NIRS channels, you can click the **View** button next to the words 'Probes and Channels', as shown in Figure 7-28, to view your settings and to verify the positions of the probes and NIRS channels.

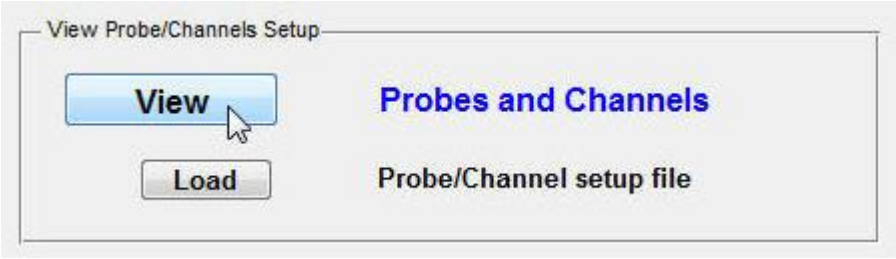


Figure 7-28. GUI for accessing display formats for assigned probe locations and channels.

Clicking on the '*View*' button brings up another GUI titled '**Probes & Channels**', having the following three functionalities:

View Probes (Default case; provides 2D/3D map of assigned optode positions)

View Channels (2D/3D map of assigned channel positions)

View Ps & Cs (Montage view of probes and channels locations)

Similar to the viewing options available for the probe and channel assignments, individual or composite views are available for viewing as either a 2D planar image or as a 3D head model. Examples of composite views for the probe arrangement listed in Figure 7-21 are shown in Figures 7-29 and 7-30 respectively.

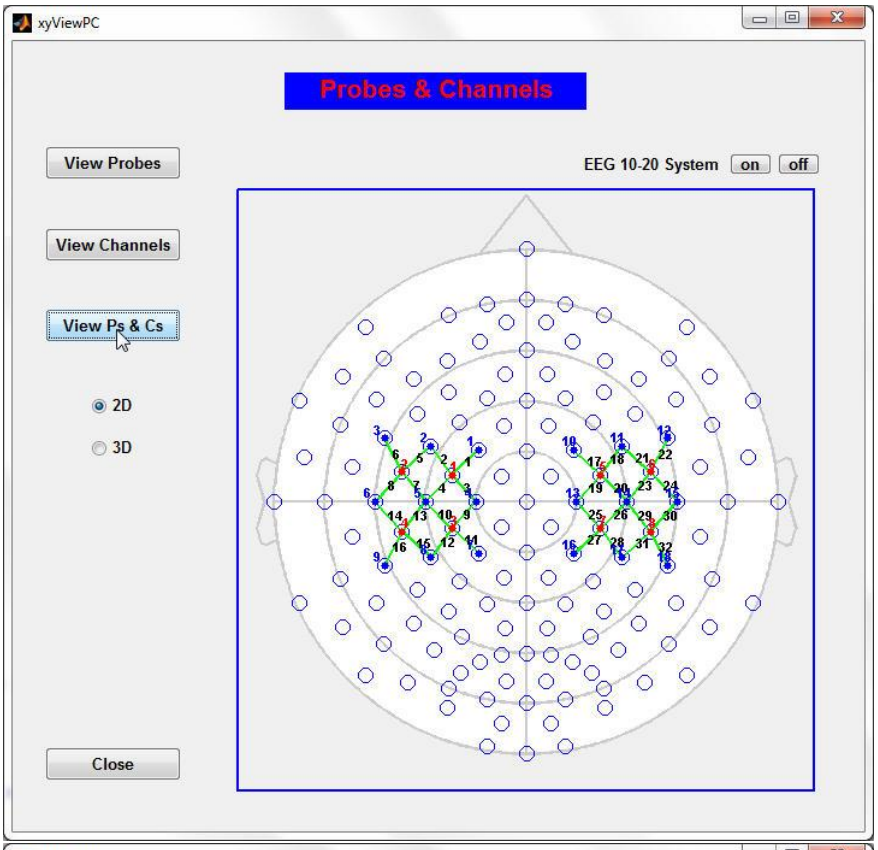


Figure 7-29: Planar composite view of assigned probe and channel positions.

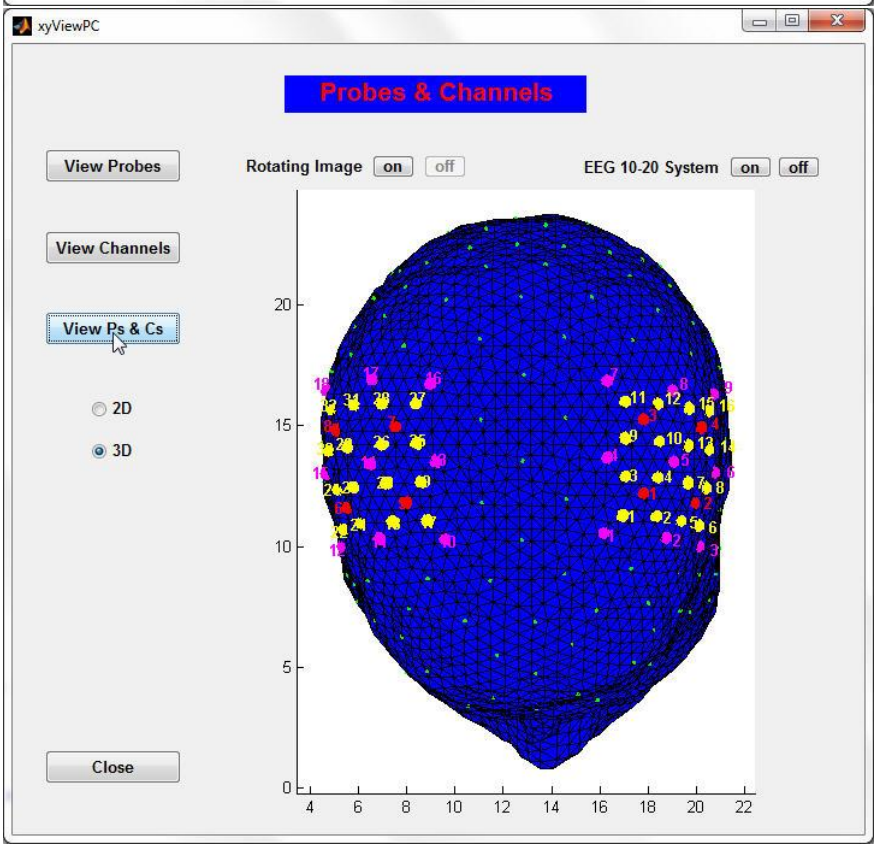


Figure 7-30: 3D head model composite view of assigned probe and channel positions.

3.1 Load probe/channel setup file

To examine a pre-existing probe setup, first load the corresponding probeInfo file and then view the probe setup as follows:

Step 1: Click the '*Load*' button next to the words 'Probe/Channel setup file' shown in Figure 28, to open a browser window which you will use to navigate to the folder where the probeInfo file is stored. Then open the probeInfo file, as shown below.

Step 2: Click the '*View*' button next to the words "Probes and Channels". By following descriptions given in Section 3 you can review a pre-existing probe setup.

3.2 Save and close probe setup

After reviewing your probe and channel assignments, click the Save button under the View Probe/Channel Setup panel in the Probe Setup GUI to save your probe setup. A Help Dialog will appear identifying the file name and location.

3.3 New Files Created:

Processing of data using the 'Probes Setup' portal generates one type of saved data files;

*Filename*_probeInfo.mat

This file records all information assigned for specified source, detector and channel locations. Information stored in this file can be accessed using either the 'Load probe/channel setup ' button within the **Probes Setup** portal, Section 3.1, or by loading the file using directions outlined in Section 3 in Chapter 2, **Experimental Data and Conditions**.

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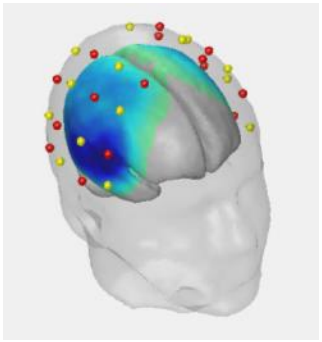
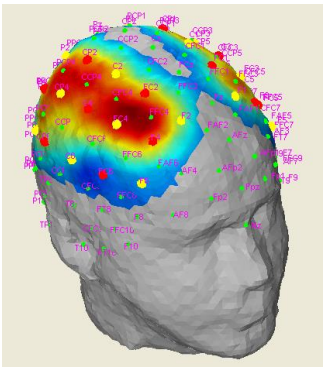
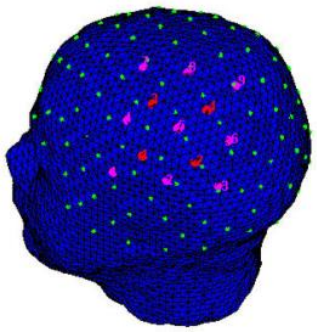
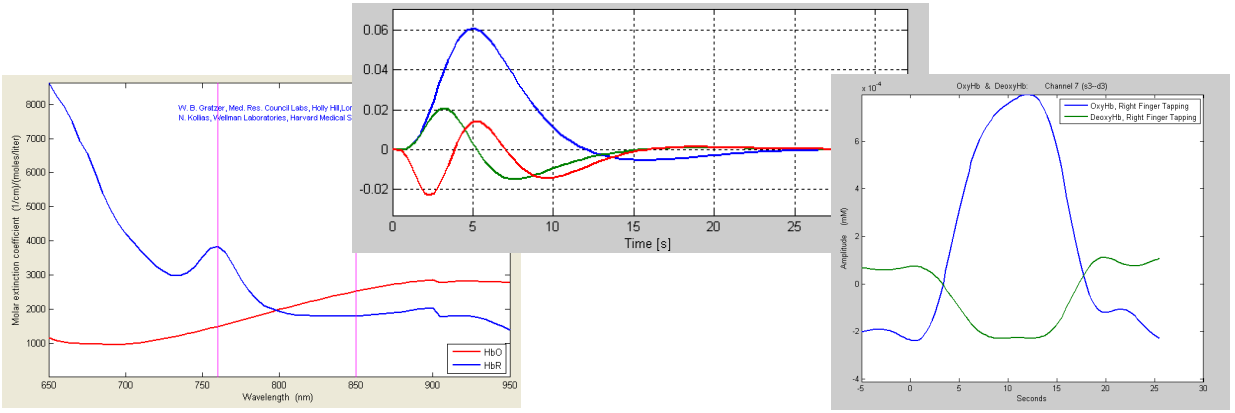
nirsLAB

Chapter 8: Data Export

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1 Introduction

nirsLab provides a **Data Export** tool in the **Utilities** portal that allows users to export nirsLab-based edited/filtered detector data and hemodynamic states (*i.e.*, oxy-Hb, deoxy-Hb, tissue blood volume, HbO_2 saturation) in ASCII format, which makes it possible for you to edit, view and analyze the exported data with other, commonly available software packages.

To launch the **Data Export** tool, first click the pull-down menu in the Utilities portal of nirsLab GUI and select the Data Export option in the menu, then click the Run button to open a new GUI named Data Export, as shown Figure 8-1.

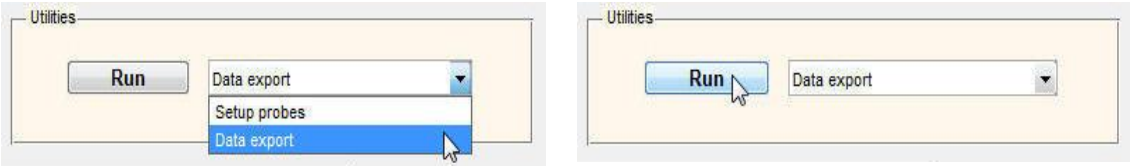


Figure 8-1. Pull down menus for Data Export

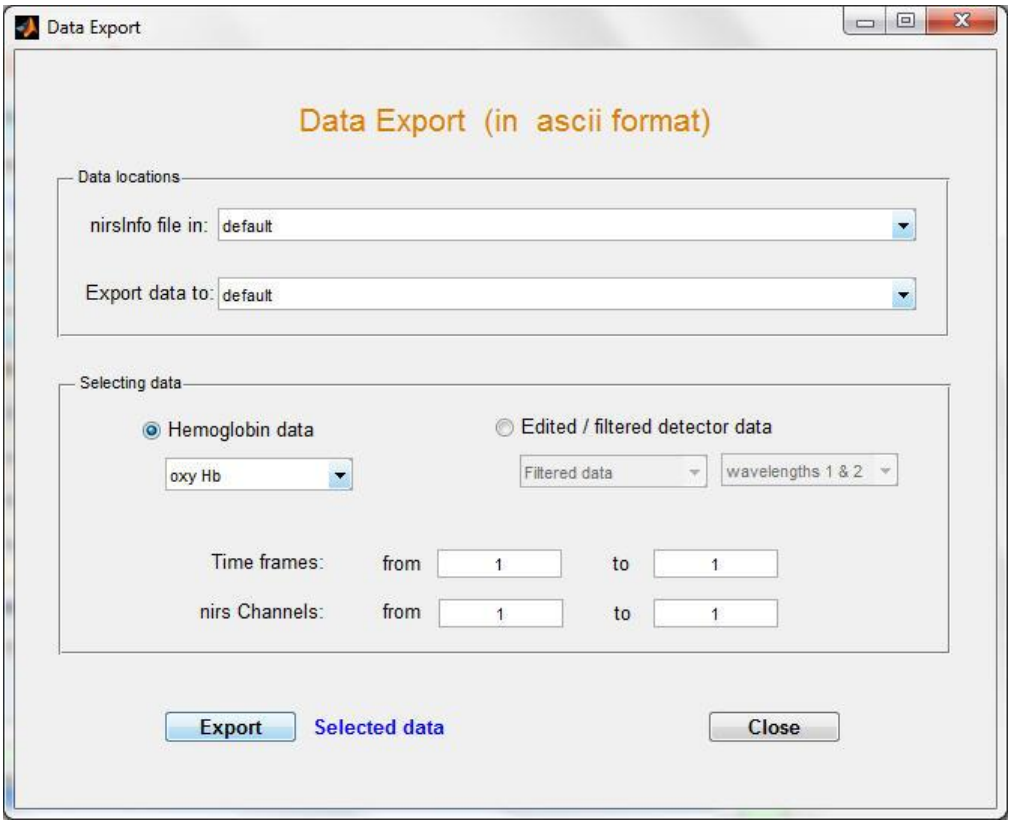


Figure 8-2. GUI for Data Export

The Data Export GUI, as illustrated in Figure 8-2, contains three basic components:

- **Data Locations:** it provides two pull-down menus for specifying where the exporting data comes from and where it to be saved.
- **Selecting data:** it provides multiple controls for selecting what data set(s) you want to export.
- **Export button:** it allows you to the specified nirsLab-based data set(s)

1.1 Access to Data Locations

The first step you need to take is to specify the project folder where the nirsLab-based data set (or the nirsInfo file) is saved, and to select the folder where you want to save the exporting data.

If a project (or a nirsInfo file) is currently being loaded in **nirsLab**, the project folder and a default folder for exporting data are automatically displayed in the two pull-down menus in the **Data Locations** portal as their first option, respectively, as the example shown Figure 8-3 illustrates.

Figure 8-3. Menu selection for data location

If no project (or nirsInfo file) has been loaded in **nirsLab**, or the data you want to export is not in the current project, take the following steps to specify or change the project folder.

1. Click on the pull-down menu next to the words "nirsInfo file in" and select the **Load a nirsInfo file** option in the menu to open a browser window, as shown in Figure 8-4.

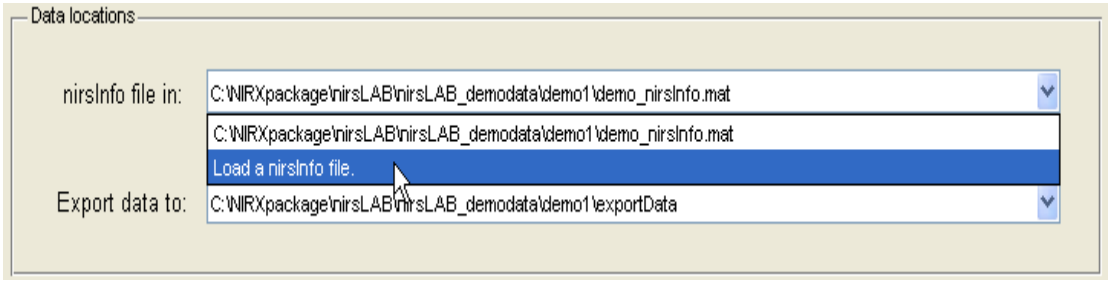


Figure 8-4. Selection of nirsInfo file.

2. Using the browser window to navigate to the desired project folder, then select the nirsInfo file in the folder and click the **Open** button to load it. After the nirsInfo file is loaded, the project folder is displayed in the pull-down menu as its first option, and choose the **exportData** folder within the project folder as the default folder to save the exporting data, which is displayed in the pull-down menu next to the words "Export data to" as its first option, as shown in Figure 8-4.

1.2 Specifying Export Data

As shown Figure 8-5, the components in the **Selecting data** portal of the Data Export GUI allow you to select the nirsLab-based data set(s) you want to export. Theses components consist of:

- **Hemoglobin data** radio button: for selecting hemodynamic states data;
- Pull-down menu for hemodynamic states: for selecting one state or multiple states;
- **Edited/filtered detector data** radio button: for selecting detector data;
- Two pull-down menus for detector data: for selecting wavelength-dependent edited or filtered detector data;
- Two **Time frames** text fields: for specifying the time interval of the exporting data;
- Two **nirs Channels** text fields: for specifying channel range of the exporting data.

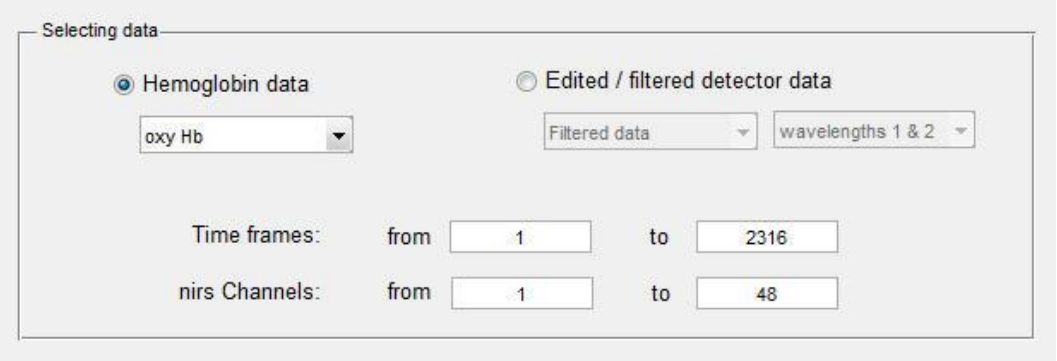


Figure 8-5. Selection options for data export.

For example, if you want to export the nirsLab-based HbO_2 saturation and filtered wavelenth-1 detector data sets that their time interval and channel range are 50-1500 and 10-30, respectively, take the following steps to specify the nirsLab-based data sets.

- Click the **Hemoglobin data** radio button and click on the pull-down menu below the radio button to select the **O2sat** option in the menu, as shown in Figure 8-6.

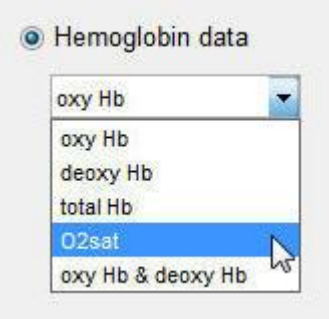


Figure 8-6. Selection of O2sat data.

- Click the **Edited/filtered data** radio button, and select the **Filtered data** option in the first pull-down menu below the radio button and the **wavelength 1** option in the second pull-down menu, as shown in Figure 8-7.

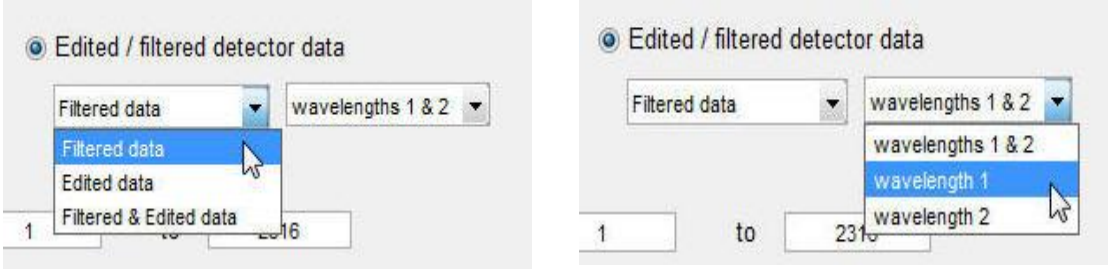


Figure 8-7. Selection of data for export.

- Type 50 and 1500 into two **Time frames** text fields, respectively.
- Type 10 and 30 into two **nirs Channels** text fields, respectively.

The specifications of the export data sets are illustrated in Figure 8-8

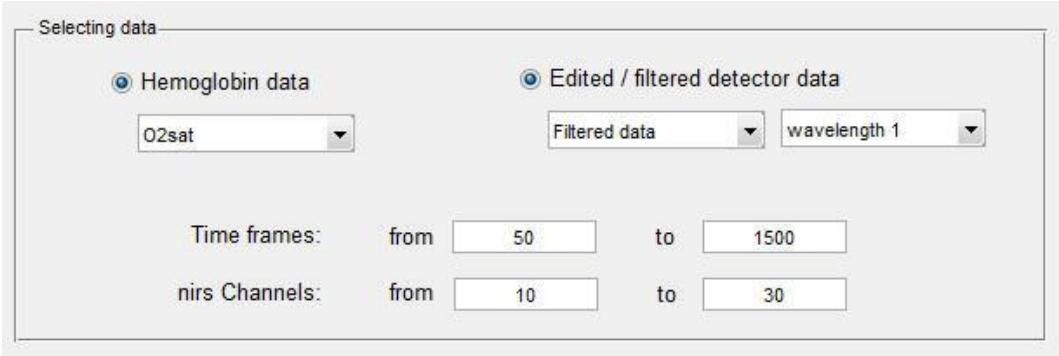
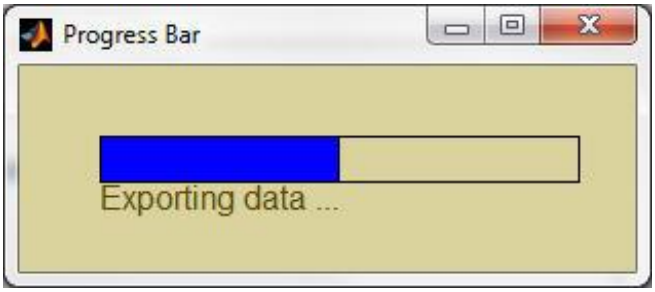


Figure 8-8. Field specification for data export.

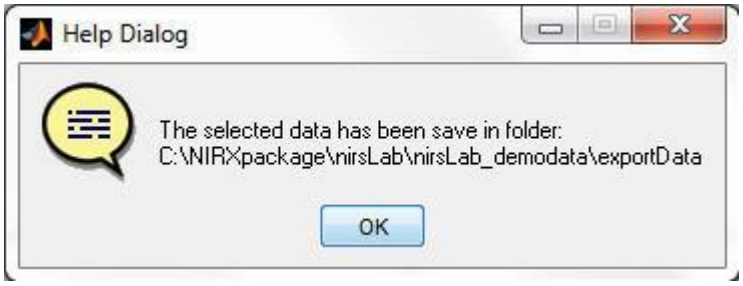
2 Exporting Data

To export the specified **nirsLab**-based data sets to the specified location, as shown below, just click the **Export** button in lower left corner of the Data Export GUI to start processing.

During the process, a progress bar appears to show how data exporting is proceeding.



After the data conversion and export process has completed a help dialogue window will open, providing information about the location of the output files.



3 Results Output

As mentioned above, after the data export process ends, the specified nirsLab-based data set(s) is automatically saved in ASCII format into the specified folder. The saved file(s) can be opened and viewed with any standard text-editing (for example, WordPad, Notepad, or Word®) or spreadsheet (for example, Excel®, PSI-Plot, ProStat) application.

In each saved file, the data is saved as a matrix. Each row contains the values of all specified channels for one time frame, and each column contains the time series for one nirs channel.

These saved files have the following file name syntax:

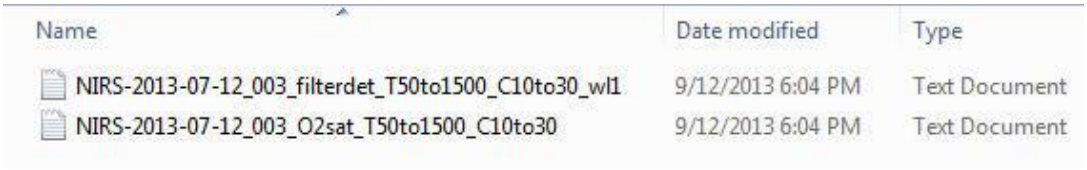
for hemodynamic state data:

[raw data file name prefix]_[state]_T(time interval)_C(channel rang).txt

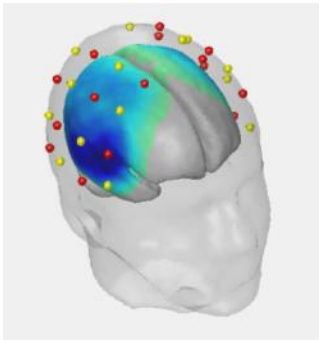
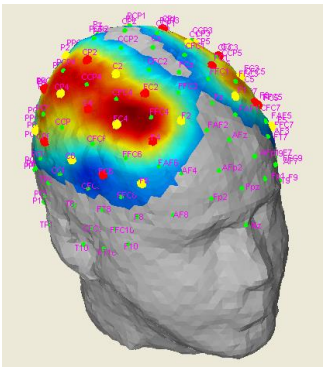
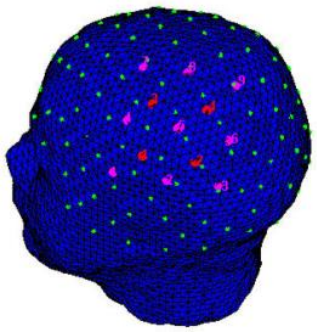
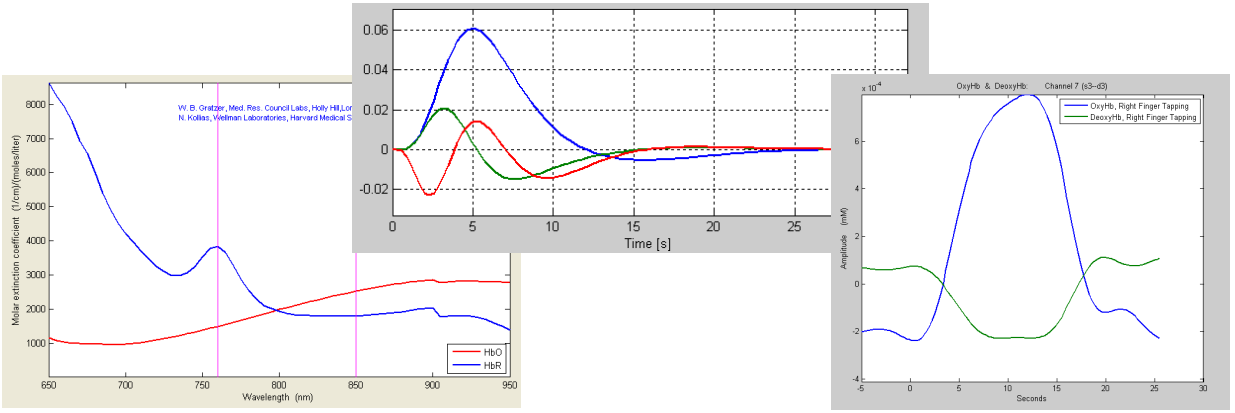
for detector data:

[raw data file name prefix]_[detector data]_T(time interval)_C(channel rang)_[wl1/wl2].txt

An example of the folder where the export data saved and the exported data files in the folder is shown in following figures.



nirsLAB

Chapter 9: Raw Data Editor

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1 Introduction

The nirsLab application provides a 'Raw Data Editor' tool in the **Utilities** portal, which allows users to reduce the size of experimental data sets recorded by NIRScout, NIRSport or DYNOT imager. The edited data sets can then be analyzed directly by nirsLAB. The editing capabilities provided are:

(1) Selection of relevant time segments from a longer time series.

(2) Downsampling of a data set by applying a temporal averaging process.

To launch the data editing tool, select the 'Raw data editor' item from the drop-down menu in the **Utilities** portal of the nirsLab GUI, as shown in Figure 9-1. Then click on the *Run* button to launch a new GUI named **Raw Data Editor**, as shown in Figure 9-2.

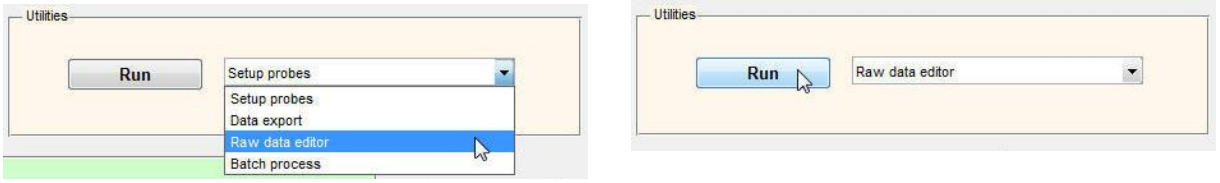


Figure 9-1. Selecting 'Raw data editor' from the drop-down menu in the nirsLAB **Utilities** portal.

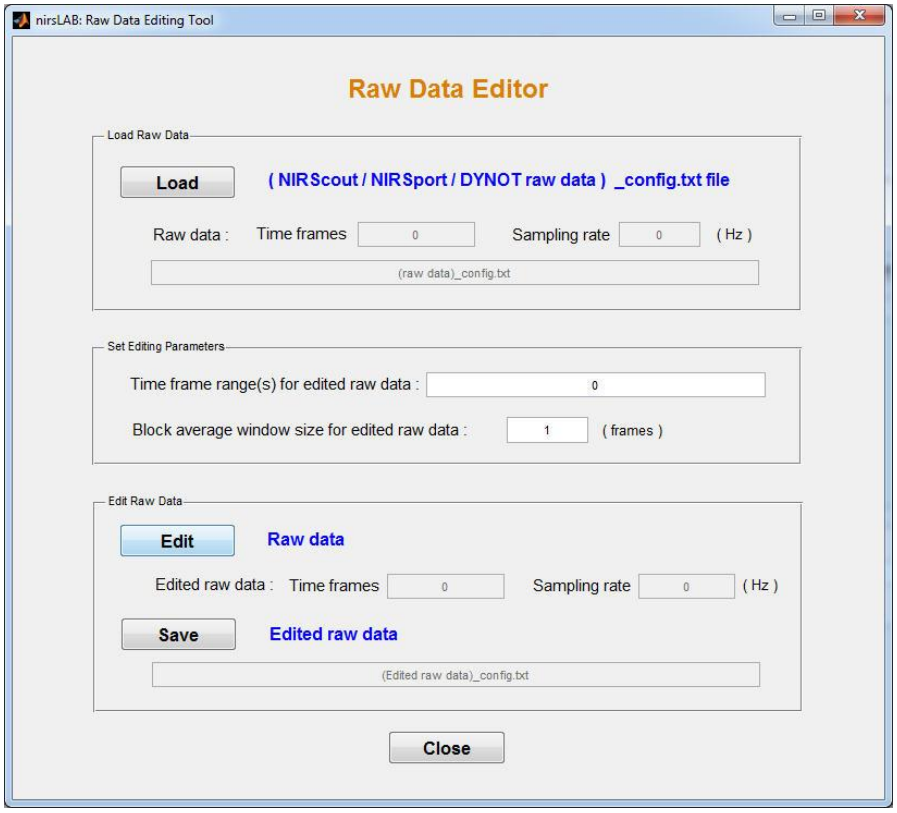


Figure 9-2. The **Raw Data Editor** GUI.

The Raw Data Editor GUI (Figure 9-2) contains three basic components:

- 'Load Raw Data' module: This is used for selecting a raw dataset that you wish to edit. After one is loaded, its name and drive location, the number of measurement time frames, and the data sampling rate are displayed in the provided text fields.
- 'Set Editing Parameters' module: This contains two editable number fields, which you can use to specify which time segments you wish to retain, and/or the size of the time window you wish to use for downsampling.
- 'Edit Raw Data' module: This contains the controls that you will use to perform the specified editing operations, and to save the edited data set.

2 Loading Raw Data

To load a data set for editing, click on the *Load* button in the 'Load Raw Data' module of **Raw Data Editor** GUI. This action will launch a browser window (Figure 9-3), which you can use to navigate to the folder where the files generated by a NIRx imager system (Chap. 1, Section 5.1) are stored. Select the file whose name ends in '_config.txt' (to assist you in this, by default nirsLAB will display only those files that have '_config' in their names). Click on the *Open* button, and the editor will automatically load all of the essential files in the data set.

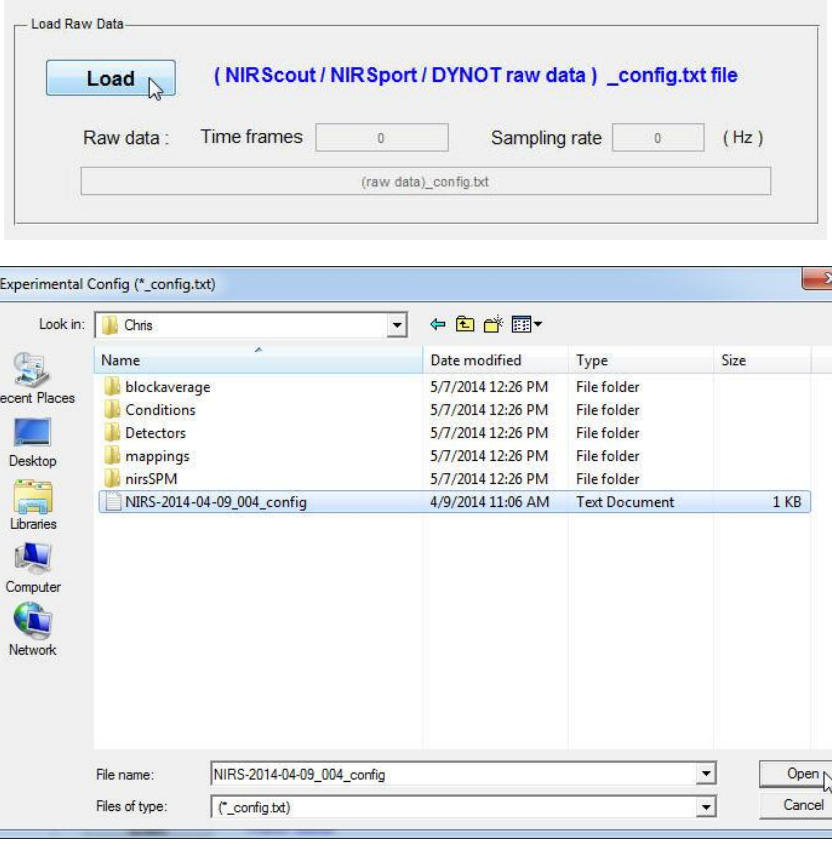


Figure 9-3. Loading the _config.txt file for an experimental data set.

After the data files have been loaded, the total number of time frames, the data sampling rate, and the location and name of the data set will be displayed in the 'Load raw Data' module's text fields, as illustrated in Figure 9-4. The sampling rate and number of time frames are also displayed in the corresponding fields of the 'Edit Raw Data' module (Figure 9-2). The reason why nirsLAB displays the same information twice in the same GUI is given below, in Section 4.

Figure 9-4. Displayed time-frame number, sampling rate, and file location.name information for the loaded data set.

3 Setting Editing Parameters

There are two kinds of editing parameters that users may specify.

- The time frames of the original data set that will be retained in the edited data set.
- The number of successive time frames from the original data set that will be averaged together to generate each new data value in the downsampled data set.

As shown in Figure 9-5, the default time frame range is the entire range of time frames in the loaded data files, and the default average window size is 1 time frame. If you do not change either parameter, then the edited data files will be identical to the ones that you loaded!

Set Editing Parameters
Time frame range(s) for edited raw data :
[1:2713]
Block average window size for edited raw data :
1
(frames)

Figure 9-5. Default data-editing parameters.

Directly type the values you want for the retained time frames and averaging/downsampling window size in the number fields seen in Figure 9-5. As a demonstration, suppose that we want to:

1. keep the first 500 time frames, discard frames 501 through 999, keep frames 1000 through 2700, and discard frames 2701 through 2713;

2. downsample the data by a factor of 3 (*i.e.*, the first data value in the edited/new data set will be the average of data from frames 1-3 of the original data set, the second new value will be the average of data from frames 4-6 of the original set, etc.).

To implement these selections, simply type '[1:500 1000:2700]' in the 'Time frame range(s) for edited raw data:' field, and '3' in the 'Block average window size for edited raw data:' field, as shown in Figure 9-6.

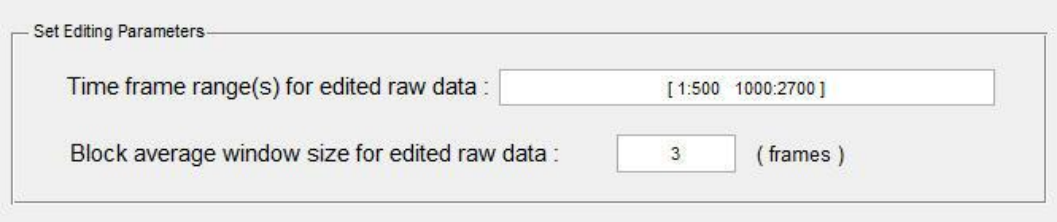

Set Editing Parameters
Time frame range(s) for edited raw data :
[1:500 1000:2700]
Block average window size for edited raw data :
3
(frames)

Figure 9-6. Modifying the data-editing parameters.

4 Editing and Saving Raw Data

When the editing parameters are set, the number of time frames and sampling rate information editor will automatically be updated in the 'Edit Raw Data' module, as shown in Figure 9-7. In this example, the edited data set has a sampling rate of 1.3033 Hz (*i.e.*, 3.91 ÷ 3 = 1.3033) and 734 time frames (*i.e.*, 1:500 = 500 and 1000:2700 = 1701 time frames, 500 + 1701 = 2201, and 2201 ÷ 3 = 734). However, the corresponding fields in the 'Load Raw Data' module are not updated. This allows you to directly compare the time-series lengths and sampling rates of the original and edited data sets.

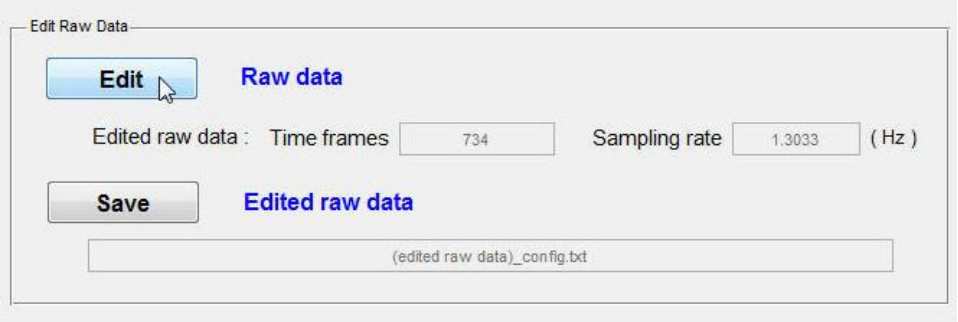


Figure 9-7. Editing raw data.

When you click on the *Edit Raw data* button in the 'Edit Raw Data' module (Figure 9-7), the editing operation(s) you have specified will be performed. The *filename*.wl1, *filename*.wl2, *filename*.evt, and *filename*_config.txt (see Chap. 1, Section 5.1) all are modified as needed during this process. As illustrated in Figure 9-8, a progress bar will pop up on your screen, to give you a graphical indication of the percentage of the editing process that has been completed.

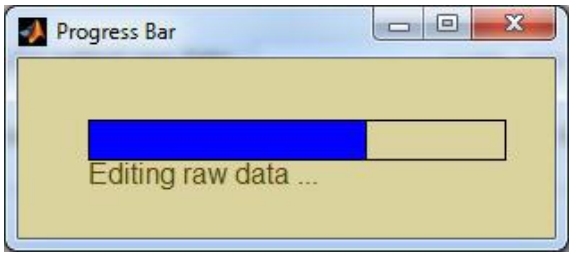


Figure 9-8. Progress bar that pops up when you click on the *Edit Raw data* button seen in Figure 9-7.

To save the edited data set, click on the *Save Edited raw data* button in the 'Edit Raw Data' module (Figure 9-9, top). This action will launch a navigator window (Figure 9-9, bottom), which you can use to select a folder as the location for the edited data set, and to specify a file name for the edited data files. As shown in Figure 9-9, the default location is a sub-folder named 'edited_rawdata', which nirsLAB will create under the folder that contains the original files, and the default file name is formed by adding the prefix 'ed_' to the original *filename*. Click on the *Save* button in the browser window to save the edited data files in the location that you have specified.

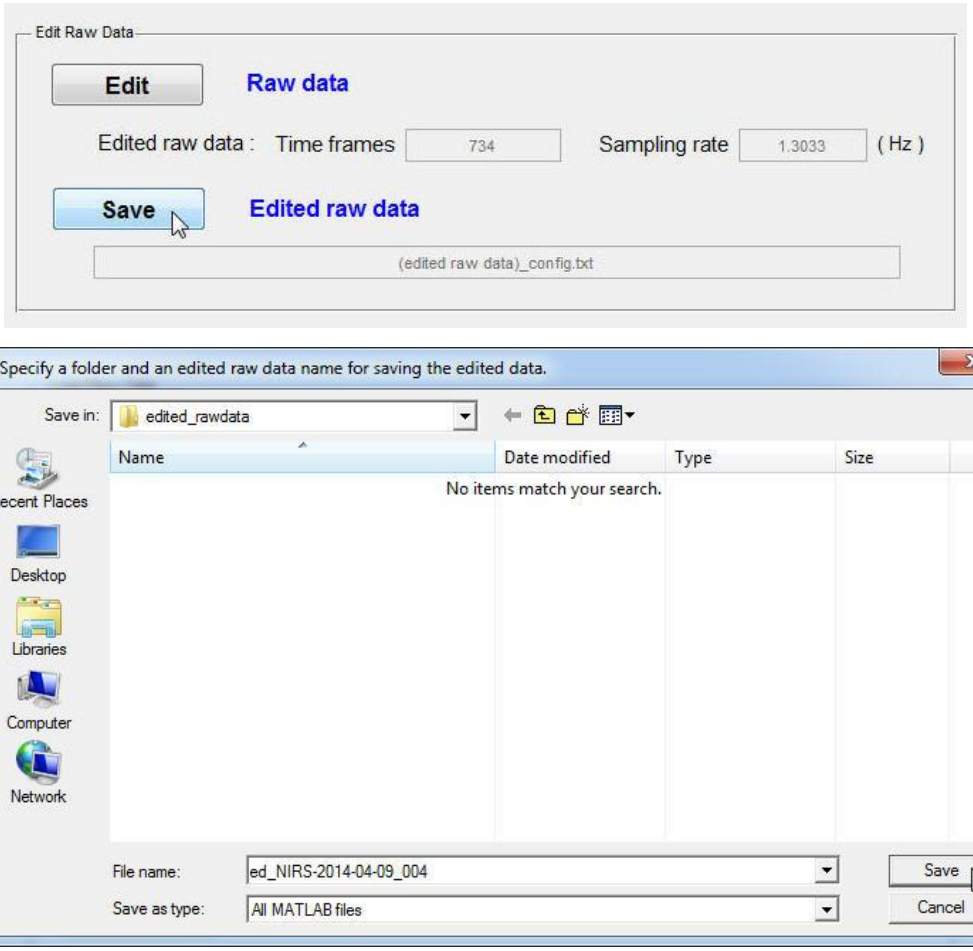


Figure 9-9. Saving an edited data set.

As illustrated in Figure 9-10, a progress bar will pop up on your screen, to give you a graphical indication of the percentage of the editing process that has been completed.

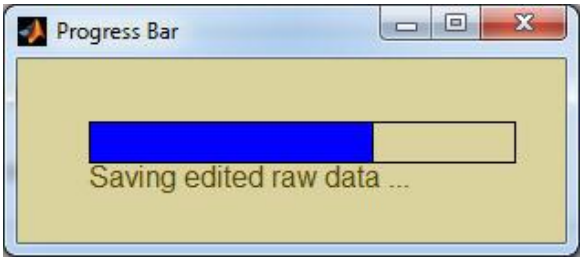
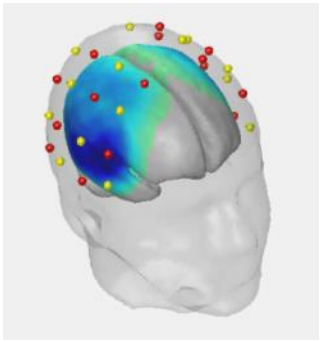
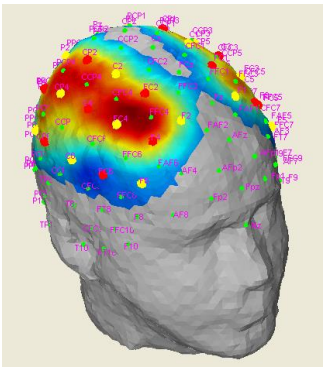
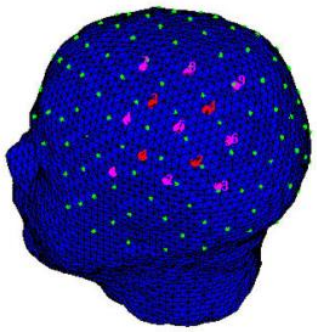
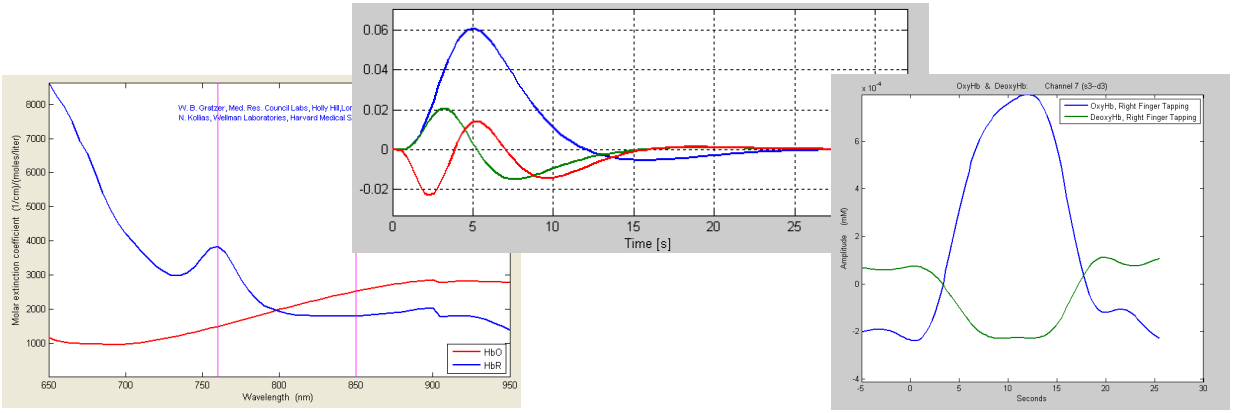


Figure 9-10. Progress bar that pops up when you click on the *Save Edited Raw data* button seen in Figure 9-9.

After the data saving process has completed, a help dialogue window will pop open your screen, confirming that the edited data files have been saved and providing information about their location.

Figure 9-11. Help dialogue window that pops up after the *Save Edited Raw data* operation is complete.

nirsLAB

Chapter 10: Batch Processing

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1 Introduction

The nirsLab application provides a 'Batch process' tool in the **Utilities** portal, which allows users to analyze a goup of experimental data sets recorded by a NIRx imager system in a single operation. In this way the total number of nirsLAB processing steps that the user needs to perform can be substantially reduced. The batch processing capabilities include:

(1) Computation of hemodynamic states for a group of subjects.

(2) Computation of Level-1 SPM results for a group of subjects (under development).

Use of the batch processing mode is appropriate and can be successfully implemented if a number of important assumptions are satisfied:

1. You have multiple data sets that all made use of the same probe layout. The 'Batch process' tool applies the same probeInfo file to all data sets in the group that you specify.
2. A single set of data-quality criteria (*i.e.*, gain-setting threshold and/or CV threshold; see Chapter 3, Section 1) is appropriate for all of the data sets in the group.
3. A single set of frequency-filtering parameters (Chap. 3, Section 4) is appropriate for all of the data sets in the group.
4. A single set of background tissue values, differential pathlength factors, and molar extinction coefficients (Chap. 4, Section 2) is appropriate for computing the hemodynamic states for all of the data sets in the group.
5. It is not necessary to apply the truncation (Chap. 3, Section 2) or artifact-reduction (Chap. 3, Sections 3 and 4) preprocessing operations to any of the data sets in the group. Since it is highly unlikely that the relevant time intervals would be the same for different data sets in the group, at this time it is necessary to process the data sets individually if you are going to truncate the data or correct for artifacts.

If you determine that batch processing is appropriate, then the basic strategy for performing it is that you:

1. Select one data set from the group and process it as described in Chapters 2-6 of this user's manual.
2. Use the 'Batch process' tool to load the _nirsInfo.mat for the selected data set and the _config.txt files for all the other data sets in the group.
3. The tool will process all of the data sets that you specify in Step 2, using the same data-quality, frequency-filtering, and hemodynamic-states parameters that you used for the data set selected in Step 1.

To launch the batch processing tool, select the 'Batch process' item from the drop-down menu in the **Utilities** portal of the nirsLab GUI, as shown in Figure 10-1. Then click on the *Run* button to launch a new GUI named **Batch Process**, as shown in Figure 10-2.

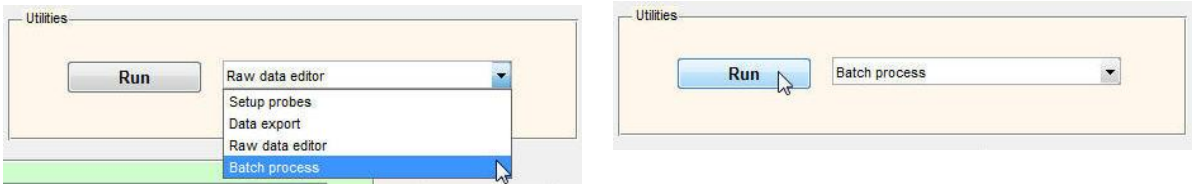


Figure 10-1. Drop-down menus for the 'Batch process' utility

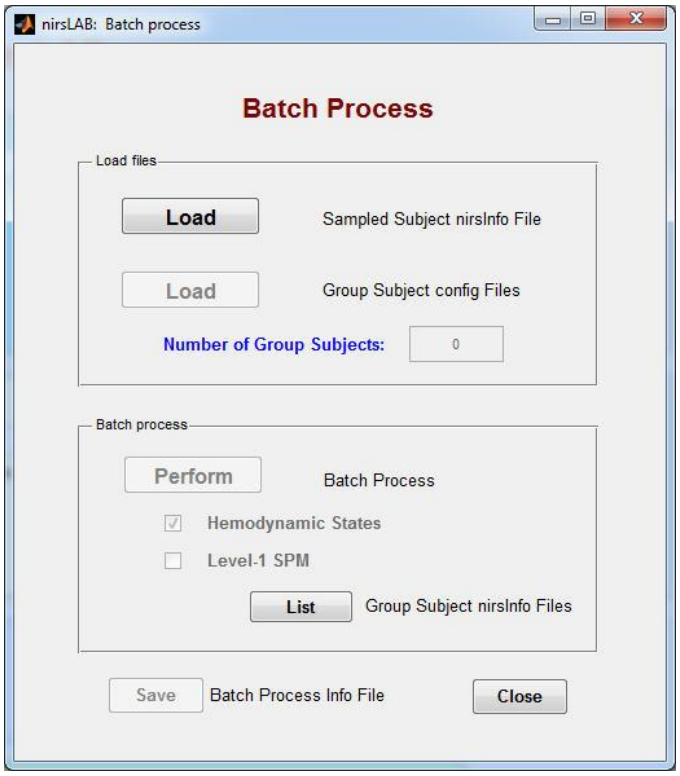


Figure 10-2. The **Batch Process** GUI.

The **Batch Process** GUI (Figure 10-2) contains three basic components:

- 'Load files' module: This is used for selecting the nirsInfo file for the data set that was processed in the conventional manner, and for selecting the config files for the remaining data sets in the group. An editable number field, in which you indicate the number of config files that will be loaded, also is provided.
- 'Batch process' module: This is used for selecting the computation(s) that you want the 'Batch process' tool to perform (however, the 'Level-1 SPM' option is not enabled in the current release of nirsLAB). There also is a button (*Perform Batch Process*) for starting the computation

sequence, and another (*List Group Subject nirsInfo Files*) that opens a window in which you can list the names and locations of the data sets that are included in the group.

- *Save Batch Process Info File* button: This allows you to save a file containing the names and locations of the data sets that are included in the group, for future reference.

2 Loading Files

2.1 Loading nirsInfo File for a Single Data Set

As indicated in Section 1, the first step in batch processing is to load the nirsInfo file that you have generated for one selected data set in the group. To do this, click on the *Load Sampled Subject nirsInfo File* button in the 'Load files' module of **Batch Process** GUI, as shown in Figure 10-3. This action will launch a browser window, which is used to navigate to the folder where the nirsInfo file for the selected data set is stored. Select the file whose name ends in '_nirsInfo.mat' from the folder. Click on the *Open* button to load the file.

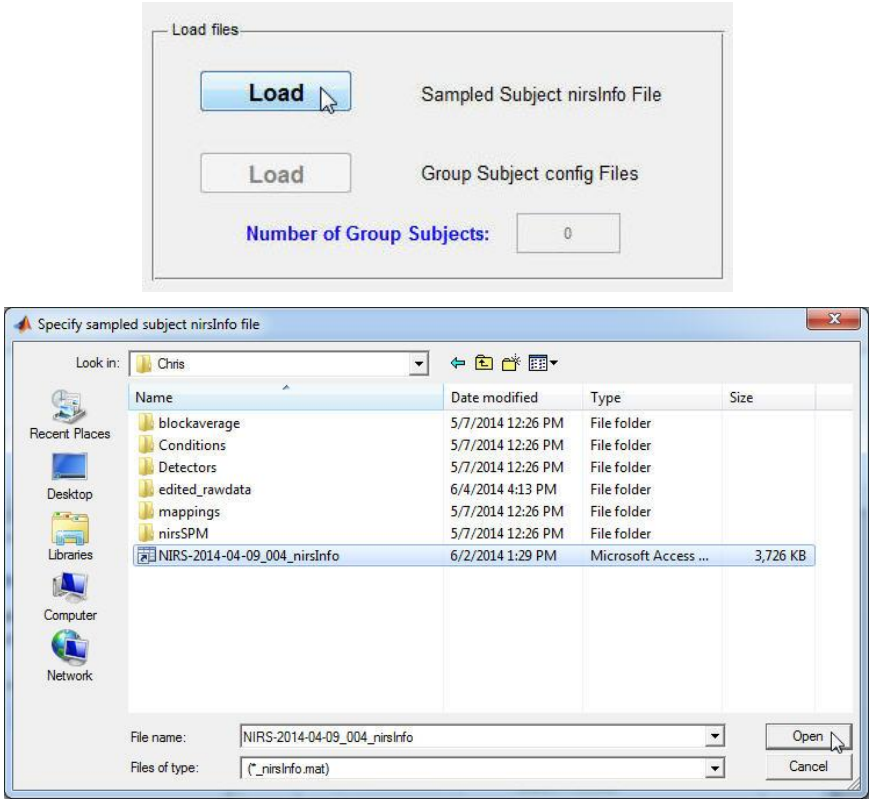


Figure 10-3. Loading the nirsInfo file for the first data set in the batch-processing group.

After the nirsInfo file has been loaded, the *Load Group Subject config Files* button and the number field for specifying the remaining number of data sets in the group, both of which are initially grayed out (Figure 10-3), will automatically become enabled, and a help dialogue window (Figure 10-4) will open to notify you that the first loading operation is complete and what must be done next.

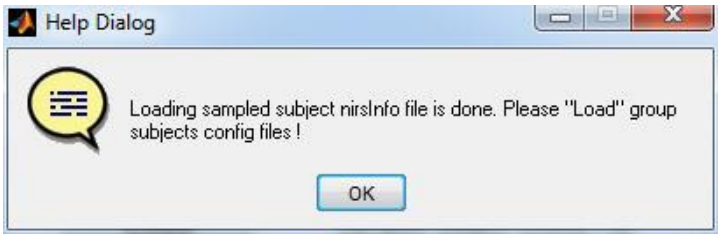


Figure 10-4. Help dialogue window that pops up after the *Load Sampled Subject nirsInfo File* operation is complete.

2.2 Loading config Files for the Batch-Processing Group

The second step in batch processing is to load the config files for all of the other data sets in your group. Begin by specifying the number of config files that you are going to load, in the 'Number of Group Subjects:' number field (3, in the example shown in Figure 10-5; and note that the number of config files is always one less than the total number of data sets in the group). Then click on the *Load Group Subjects config Files* button. This action will launch a browser window, as shown in Figure 10-5.

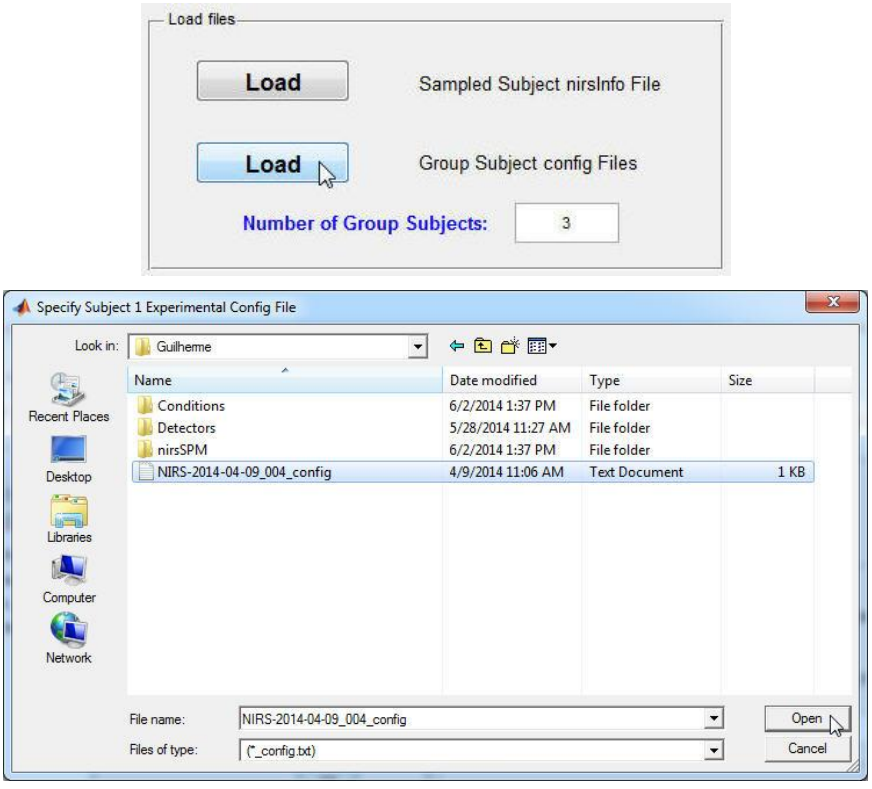


Figure 10-5. Loading the nirsInfo file for the first data set in the batch-processing group.

As indicated above, the number of group subjects is 3 in this example (Figure 10-5). Use the browser window to navigate to the folder where the raw data files for any of those data sets are stored, select the file whose name ends in '_config.txt' from that folder, and click on the *Open* button to load the data set and generate a corresponding nirsInfo file. A progress bar will pop open on your screen, to give you a graphical indication of the percentage of the process that has been completed (Figure 10-6).

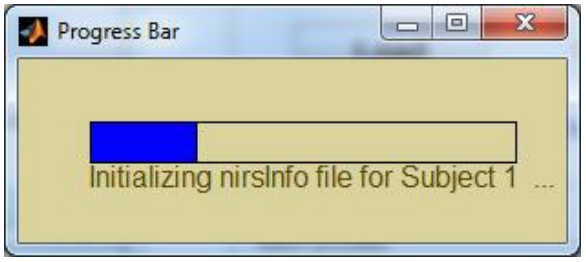


Figure 10-6. Progress bar that pops up when you select a config file for loading, as illustrated in Figure 10-5.

When the process of loading data files and generating a nirsInfo file is complete, a window such as the one shown in Figure 10-7 will pop open. In the editable field, specify the range of data time frames that you want to use as the baseline for computing the hemodynamic states for this data set. As seen in Figure 10-7, the default baseline is the entire measurement time range.

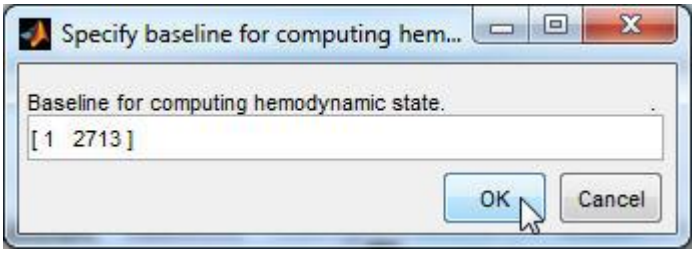


Figure 10-7. Specifying a baseline time interval.

Click on the *OK* button. This action will launch another browser window, which you will use to navigate to and load the config file for another one of the group's config files. The same sequence of steps will repeat until the files have been loaded, and nirsInfo files generated, for all of the data sets in the group. After the final data set has been processed, a help dialogue window will open, to notify you that the entire loading operation is complete and what must be done next (Figure 10-8).

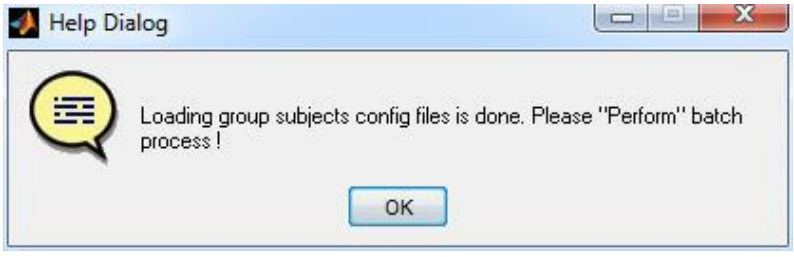


Figure 10-8. Help dialogue window that pops up after the *Load Group Subjects config Files* operation is complete.

3 Batch Processing

3. 1 Performing Batch Processing

Clicking the *Perform Batch Process* button in the 'Batch Process' module, as shown in Figure 10-9. nirsLAB will carry out the selected frequency-filtering and hemodynamic-states computations for every data set for which you have loaded a config file (Section 2.2).

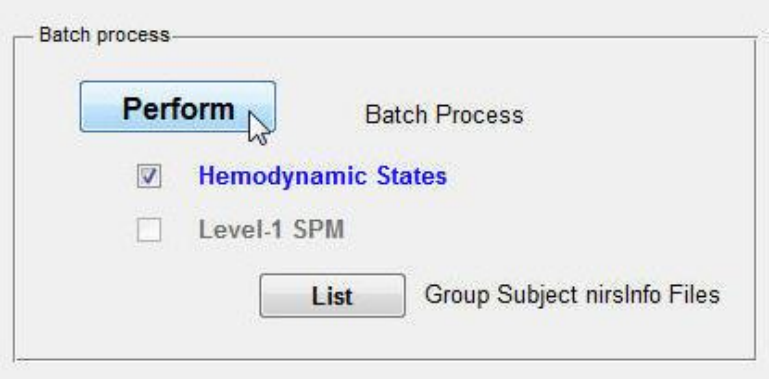


Figure 10-9. Performing the batch processing operations.

A progress bar will pop open on your screen, to give you a graphical indication of the percentage of the process that has been completed (Figure 10-10).

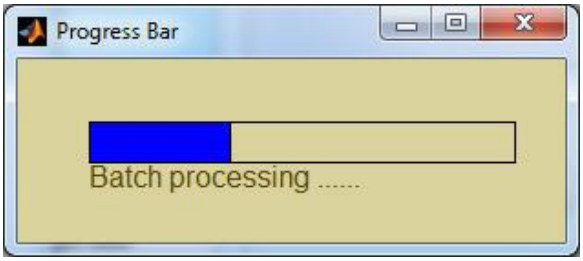


Figure 10-10. Progress bar that pops up when you click on the *Perform Batch Process* button seen in Figure 10-9.

When the batch processing is complete, each data set will have f*_filename*.dat (Chap. 3, Section 1) and h*_filename*.dat (Chap. 4, Section 4) files saved in the corresponding 'Detectors' sub-folder, and all of the information relevant to the processing steps will be saved in the corresponding nirsInfo file.

3.2 Listing Batch Processing Results

To assist in viewing batch processing results, the 'Batch process' tool provides users with the ability to generate a list of the names and locations of the data sets that were included in the group. As shown in

Figure 10-11, clicking the *List Group Subject nirsinfo Files* button will launch a new GUI, in which the names and locations of the data sets are displayed.

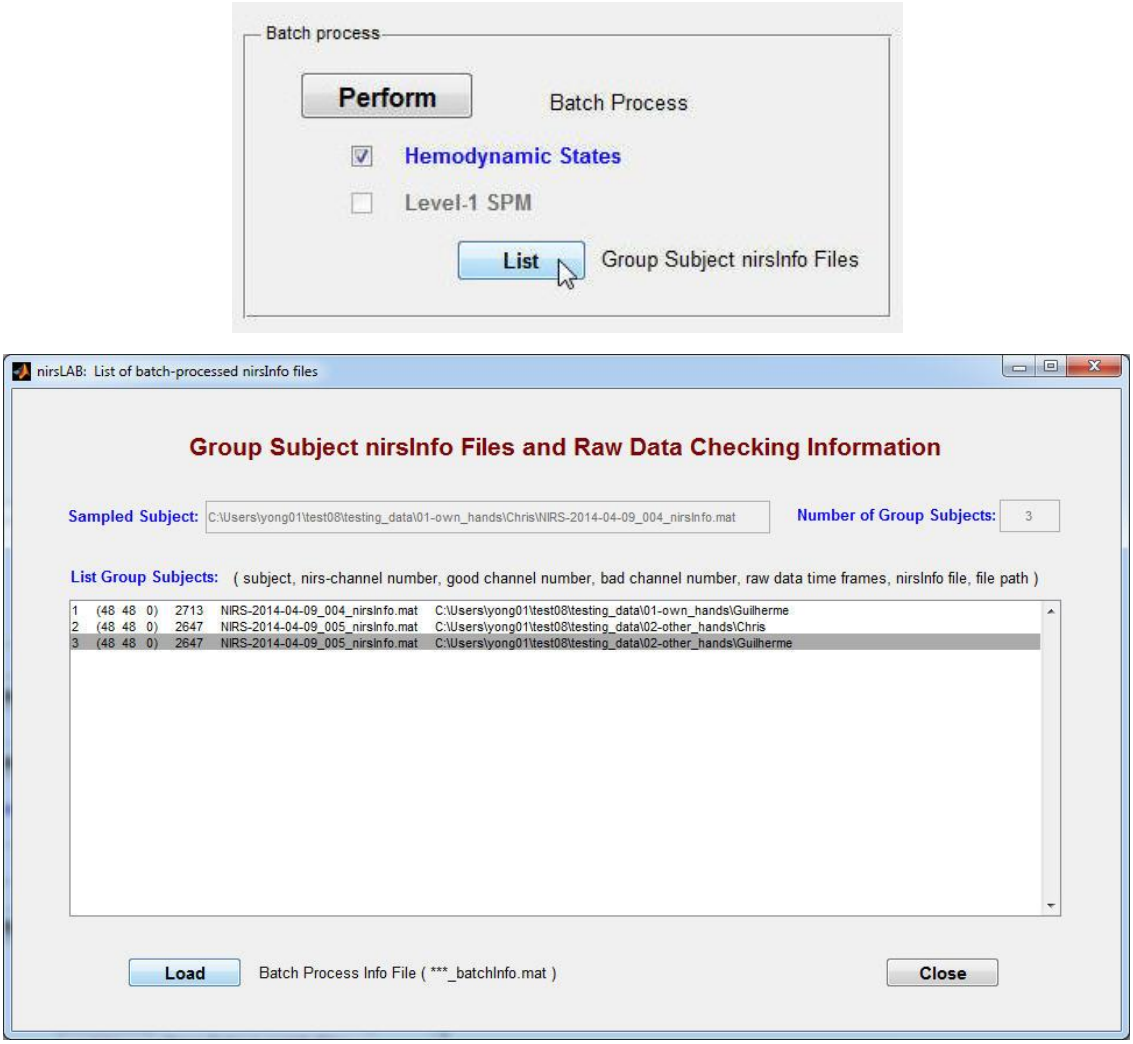
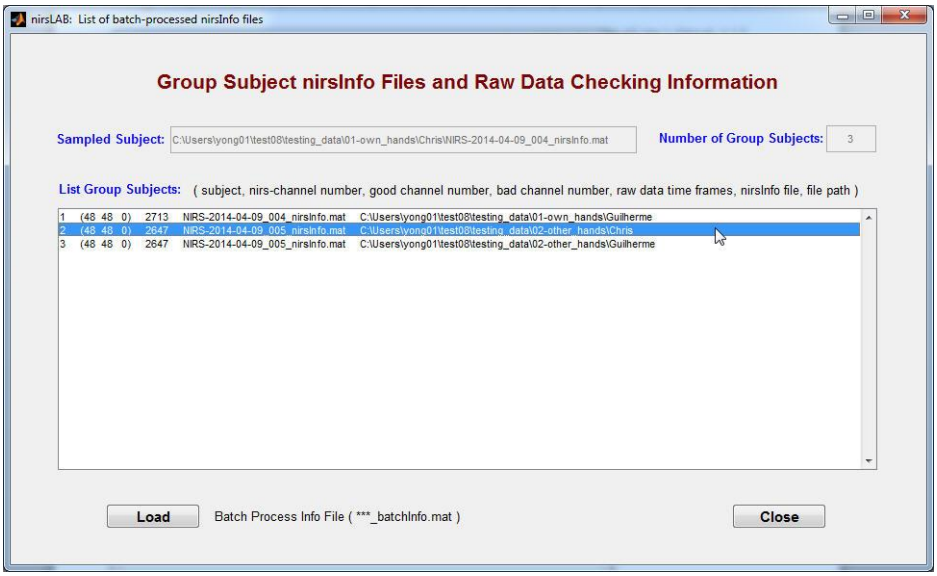

Batch process
Perform
Batch Process
Hemodynamic States
Level-1 SPM
List
Group Subject nirsInfo Files
nirsLAB: List of batch-processed nirsInfo files
Group Subject nirsInfo Files and Raw Data Checking Information
Sampled Subject:
C:\Users\yong01\test08\testing_data\01-own_hands\Chris\NIRS-2014-04-09_004_nirsInfo.mat
Number of Group Subjects:
3
List Group Subjects: (subject, nirs-channel number, good channel number, bad channel number, raw data time frames, nirsInfo file, file path)
1 (48 48 0) 2713 NIRS-2014-04-09_004_nirsInfo.mat C:\Users\yong01\test08\testing_data\01-own_hands\Guilherme
2 (48 48 0) 2647 NIRS-2014-04-09_005_nirsInfo.mat C:\Users\yong01\test08\testing_data\02-other_hands\Chris
3 (48 48 0) 2647 NIRS-2014-04-09_005_nirsInfo.mat C:\Users\yong01\test08\testing_data\02-other_hands\Guilherme
Load
Batch Process Info File (***_batchInfo.mat)
Close

Figure 10-11. Clicking on the *List Group Subject nirsInfo Files* button in the 'Batch process' module (top) launches the **Group Subject nirsInfo Files and Raw Data Checking Information** GUI (bottom).

As shown in Figure 10-11, the GUI lists the numbers of good and bad channels, the length, in time frames, of each data set, and the name and location for each nirsInfo file. If you want to use nirsLAB data viewer (Chap. 5) to plot and map the hemodynamic states for one of the data sets, simply click anywhere in the relevant batch-process information line in the GUI. This action will load the selected nirsInfo file in the nirsLAB main GUI. An example of this is shown in Figure 10-12, where the second subject in the group has been selected.


nirsLAB: List of batch-processed nirsInfo files
Group Subject nirsInfo Files and Raw Data Checking Information
Sampled Subject:
C:\Users\yong01\test08\testing_data\01-own_hands\Chris\NIRS-2014-04-09_004_nirsInfo.mat
Number of Group Subjects:
3
List Group Subjects: (subject, nirs-channel number, good channel number, bad channel number, raw data time frames, nirsInfo file, file path)
1 (48 48 0) 2713 NIRS-2014-04-09_004_nirsInfo.mat C:\Users\yong01\test08\testing_data\01-own_hands\Guilherme
2 (48 48 0) 2647 NIRS-2014-04-09_005_nirsInfo.mat C:\Users\yong01\test08\testing_data\02-other_hands\Chris
3 (48 48 0) 2647 NIRS-2014-04-09_005_nirsInfo.mat C:\Users\yong01\test08\testing_data\02-other_hands\Guilherme
Load
Batch Process Info File (***_batchInfo.mat)
Close

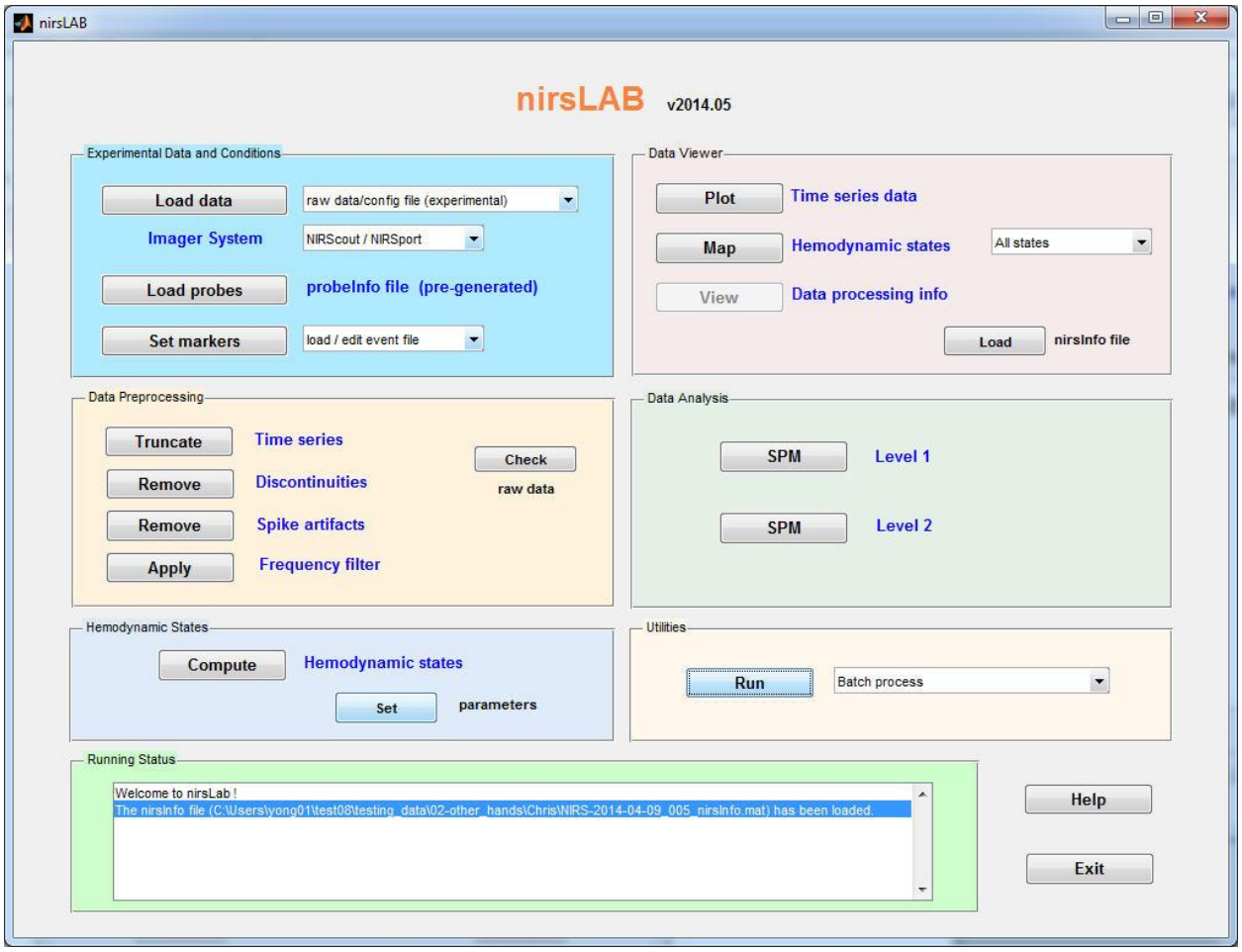


Figure 10-12. Using the **Group Subject nirsInfo Files and Raw Data Checking Information** GUI (top) to load a selected nirsInfo file into nirsLAB (bottom).

If you want to view batch processing information that was generated earlier in the nirsLAB session or during a previous one, you can click the *Load Batch Process Info File* button located at the bottom of the **Group Subject nirsInfo Files and Raw Data Checking Information** GUI (Figure 10-11) to load a previously saved batchInfo.mat file (Section 3.3). and the loaded batch process information will be listed in the GUI.

3.3 Saving Batch Processing Information

When the batch processing operations are completeed, the *Save Batch Process Info File* button at the bottom of the **Batch Process** GUI (Figure 10-13) becomes enabled. Click on the button to launch a navigator window that you can use to select a folder where you want to store the batch processing information, and to specify the file name of the file. As shown in Figure 10-13, the default location is the folder where the nirsInfo file is stored for the first data set that you loaded in the current batch process (Section 2.1), and the default file name is created by appending '_batchInfo.mat' to that data set's *filename* (*e.g.*, the default file name is 'NIRS-2014-04-09_004_batchInfo.mat' for the example used to illustrate batch processing in this chapter; you are permitted to change the file name, but please keep the '_batchInfo.mat' ending). Click on the *Save* button in the browser window, the batchInfo file will automatically be saved in your specified folder.

When the file-saving procedure is complete, a help dialogue window will open, providing information about the name and the location of the batchInfo file, as shown in Figure 10-14.

The saved batchInfo file contains the information that is shown displayed in the **Group Subject nirsInfo Files and Raw Data Checking Information** GUI in Figure 10-11. By clicking on the *Load Batch Process Info File* button (Figure 10-11; Section 3.2), you can reload the batchInfo file at a later time, and view the saved information in the manner illustrated in Figure 10-12.

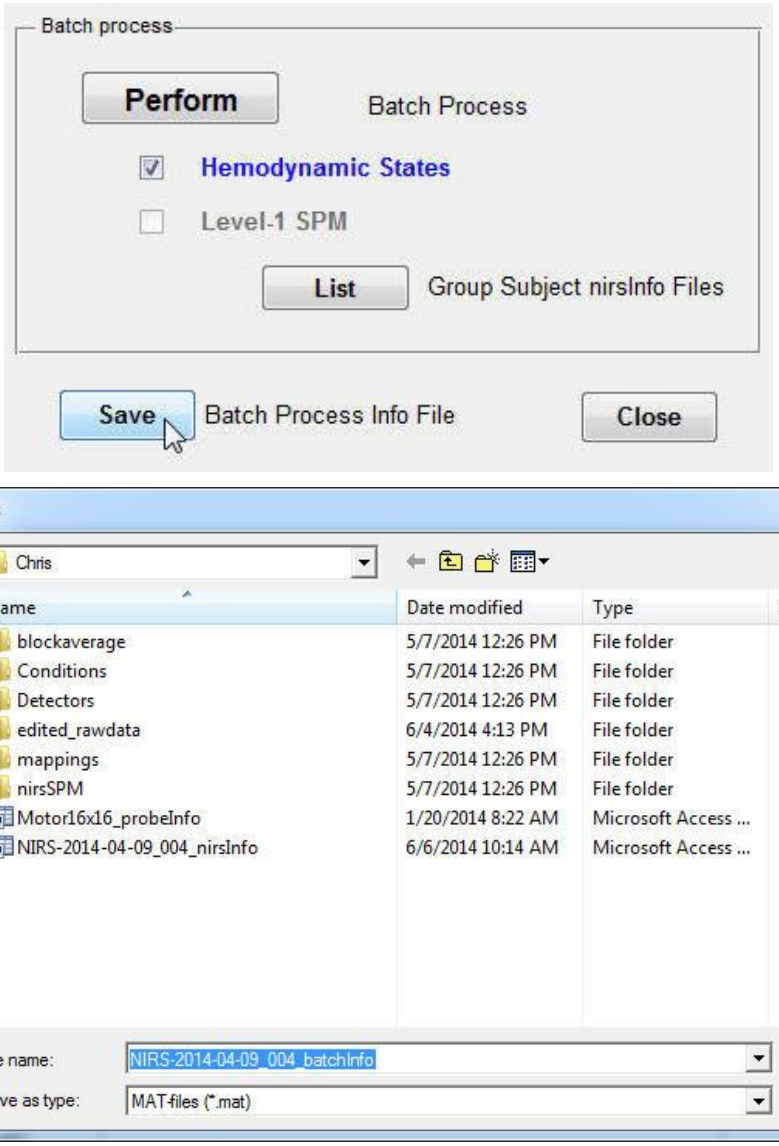


Figure 10-13. Saving batch processing information.

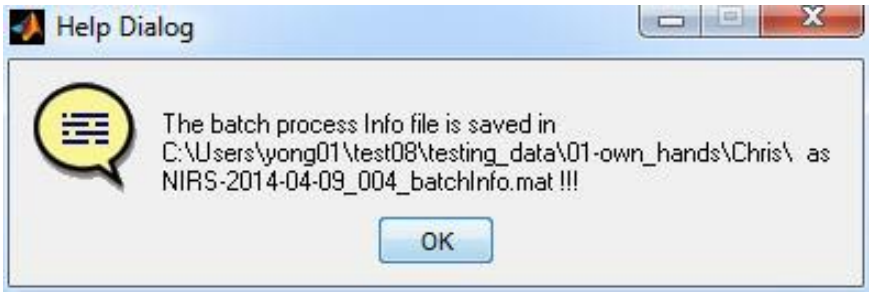


Figure 10-14. Help dialogue window that pops up after the *Save Batch Process Info File* operation is complete.